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(54) **MODELS OF ATHEROSCLEROSIS,
HYPERLIPIDEMIA, LIPOPROTEIN
OXIDATION AND BLOOD VESSEL
INFLAMMATION AND METHODS FOR
MAKING AND USING THEM**

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13, 2006.

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G01N 33/00 (2006.01)
A01K 67/00 (2006.01)
A01K 67/027 (2006.01)
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C12N 5/00 (2006.01)
C07K 14/775 (2006.01)

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CPC **A01K 67/0275** (2013.01); **C07K 14/775**
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2267/0362 (2013.01)

(58) **Field of Classification Search**
CPC **C07K 14/775**; **A01K 67/0275**
USPC **800/3**
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

2002/0049986 A1* 4/2002 Farber et al. 800/3
2004/0209279 A1 10/2004 Wu et al.
2007/0116645 A1* 5/2007 Farber et al. 424/9.2

OTHER PUBLICATIONS

Babin et al 1997, Proc. Natl. Acad. Sci. USA 9:8622-8627.*
Marza et al 2005, Developmental Dynamics 232:506-518.*
Alimuddin et al., "Enhancement of EPA and DHA biosynthesis by
over-expression of masu salmon Δ6-desaturase-like gene in
zebrafish," Trangenic Research (2005) 14:159-165.
Dias et al., "Dietary protein source affects lipid metabolism in the
European seabass (*Dicentrarchus labrax*)," Comparative Biochem-
istry and Physiology, Part A 142 (2005) 19-31.
Giffo-Schmidt, Beate, International Preliminary Examination
Report and Written Opinion, PCT/US2007/079927, International
Bureau of WIPO, Apr. 15, 2009.
Hansson et al., "The immune response in atherosclerosis: a double-
edged sword," Nat. Rev. Immunol., 508-519, Jul. 2006, vol. 6.
Hiriyanna, Kelaginamane, International Search Report, WO2008/
048773 A3, PCT/US07/79927, International Bureau of WIPO, Sep.
17, 2008.
Hiriyanna, Kelaginamane, Written Opinion, PCT/US07/79927,
International Bureau of WIPO, Jun. 18, 2008.
Ho et al., "Lipid Metabolism in Zebrafish," Methods in Cell Biology,
vol. 76, 2004, pp. 87-108.
Marza et al., "Developmental Expression and Nutritional Regulation
of a Zebrafish Gene Homologous to Mammalian Microsomal
Triglyceride Transfer Protein Large Subunit," Developmental
Dynamics, 232:506-518, 2005.
Meir et al., "Atherosclerosis in the Apolipoprotein E-Deficient
Mouse: A Decade of Progress," (2004) Atheroscler Thromb Vasc
Biol. 24:1006-1014.
Schlegel et al., "Microsomal Triglyceride Transfer Protein Is
Required for Yolk Lipid Utilization and Absorption of Dietary Lipids
in Zebrafish Larvae," Biochemistry, 2006, 45, 15179-15187.
Zon et al., "In Vivo Drug Discovery in the Zebrafish," Jan. 2005, Nat.
Review, vol. 4, pp. 35-44.

* cited by examiner

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(57) **ABSTRACT**

The invention provides genetically altered fish of the family
Cyprinidae, or genus *Danio*, including zebrafish (*Danio*
rerio) and host cells from these animals, where the fish have
been genetically altered to lack or have a modified gene
related to lipid metabolism, for example, an ApoE, ApoA1
and/or LDL-R gene. In another aspect, the invention is
directed to drug design or discovery using the animal or cell
models of the invention and/or wild type zebrafish, and by
administering an altered diet and/or environment to the ani-
mal of invention. The invention also provides methods for
screening for a compound capable of ameliorating or prevent-
ing or reversing: atherosclerosis; hyperlipidemia; lipoprotein
oxidation; the accumulation of lipid in a blood vessel wall;
vascular inflammation associated with lipid accumulation in
a blood vessel wall; acute atherosclerosis-associated events;
heart attack; stroke.

15 Claims, 12 Drawing Sheets

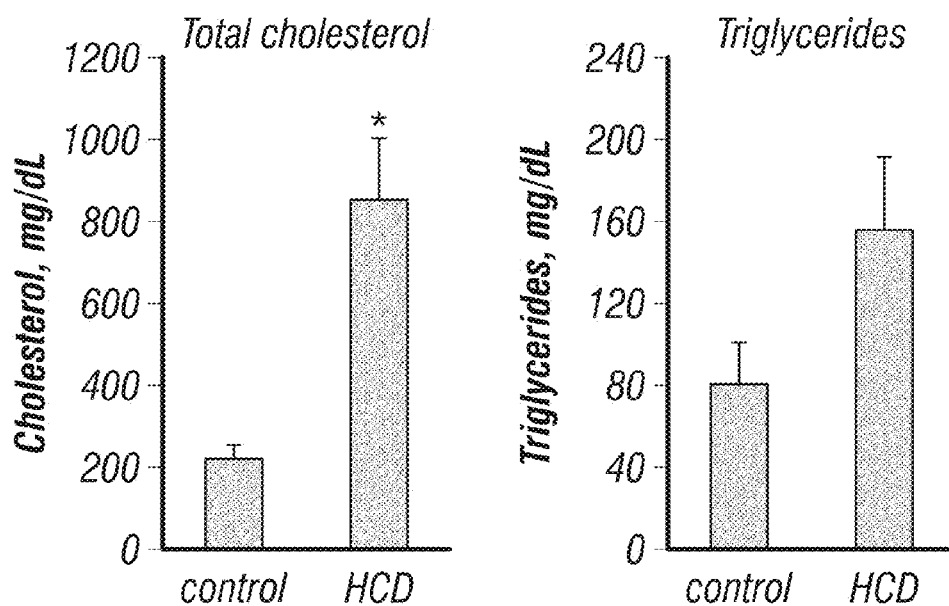


FIG. 1A

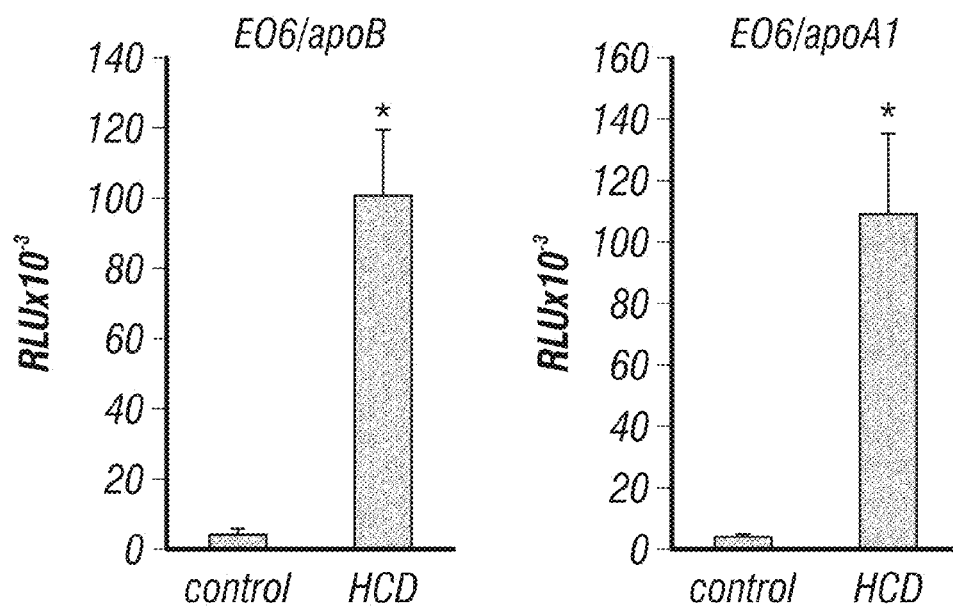


FIG. 1B

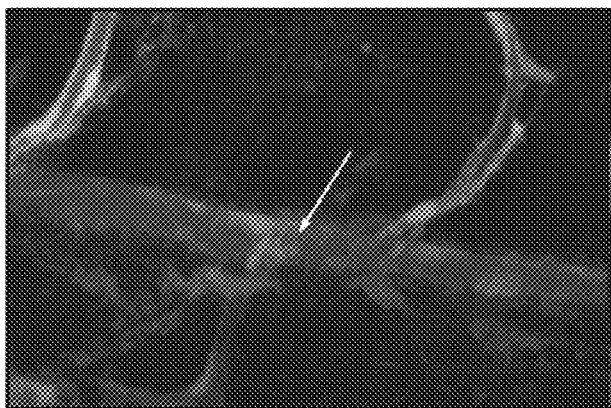


FIG. 2

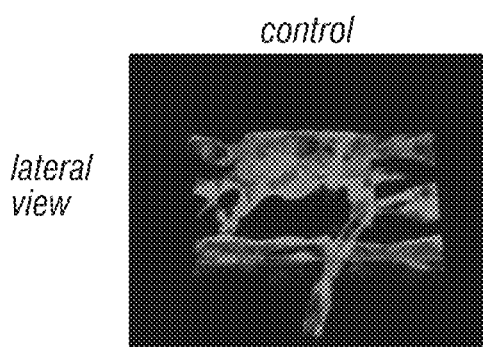


FIG. 3A

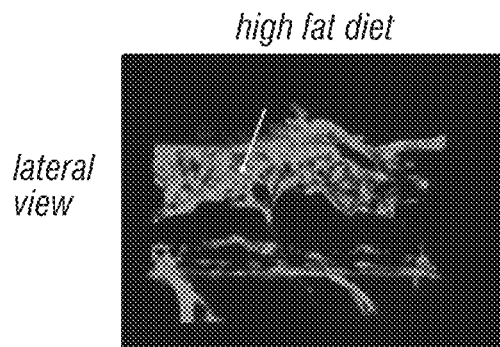


FIG. 3C

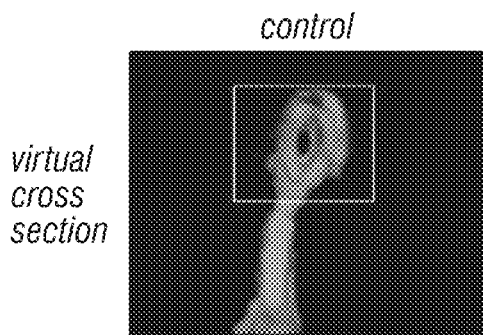


FIG. 3B

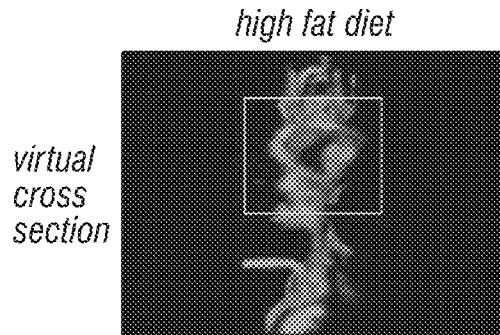


FIG. 3D

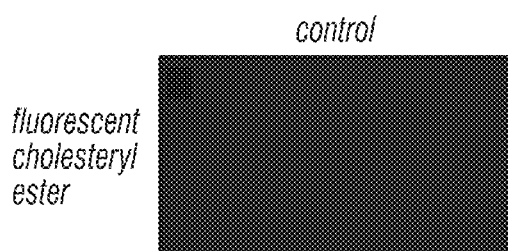


FIG. 4A

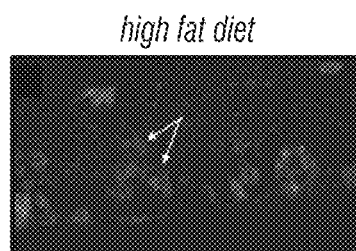


FIG. 4C

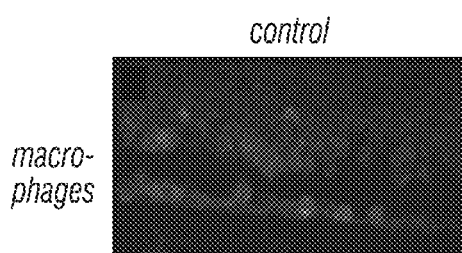


FIG. 4B

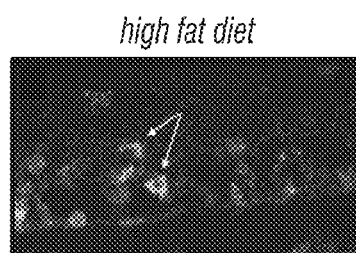


FIG. 4D

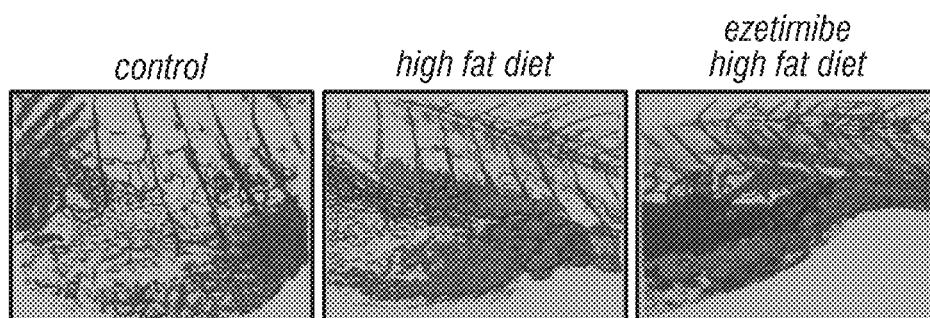


FIG. 5A

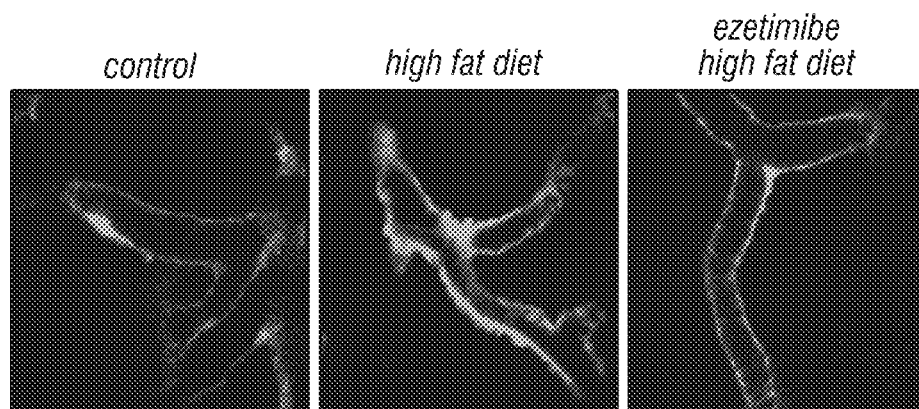
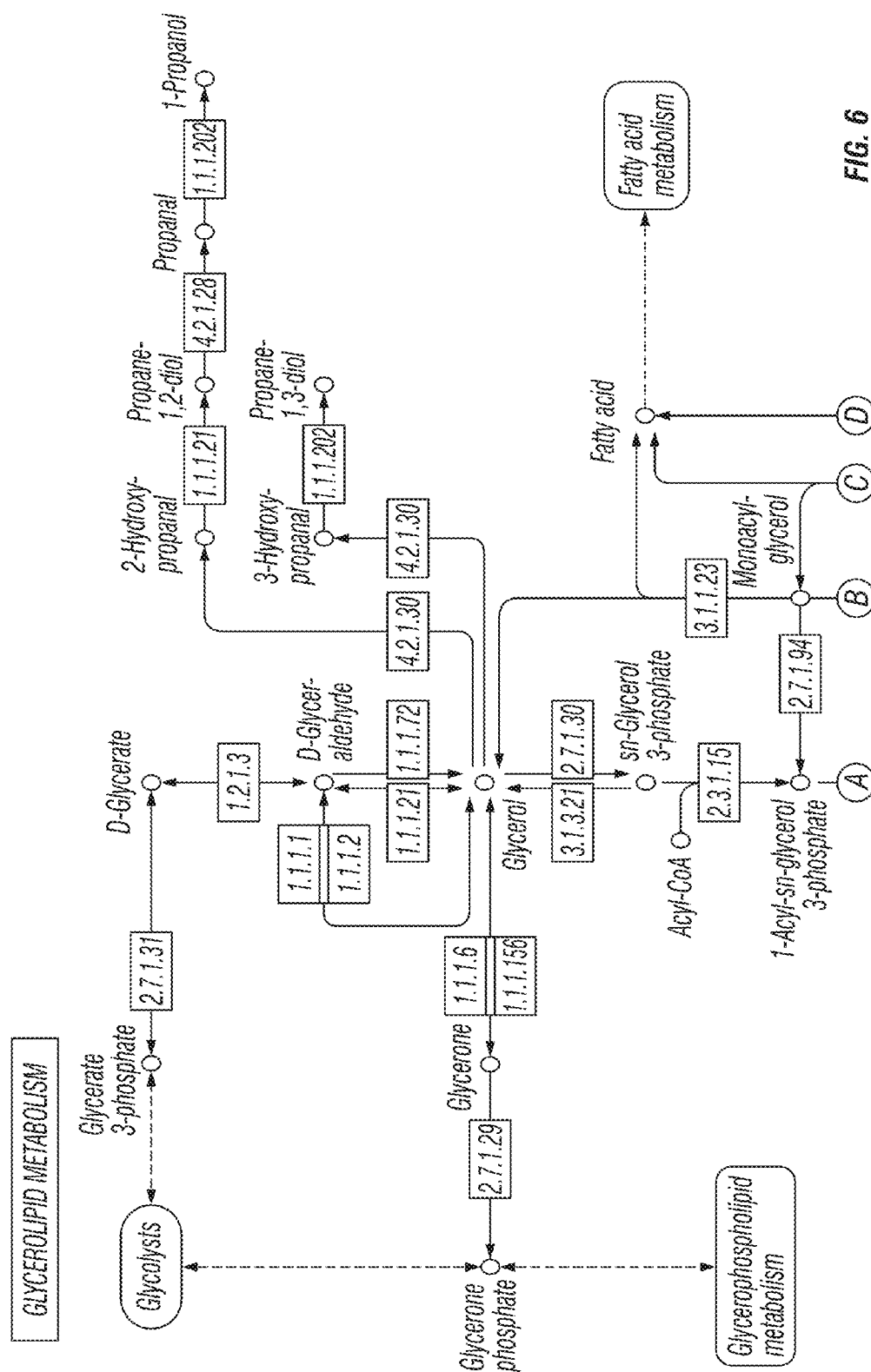
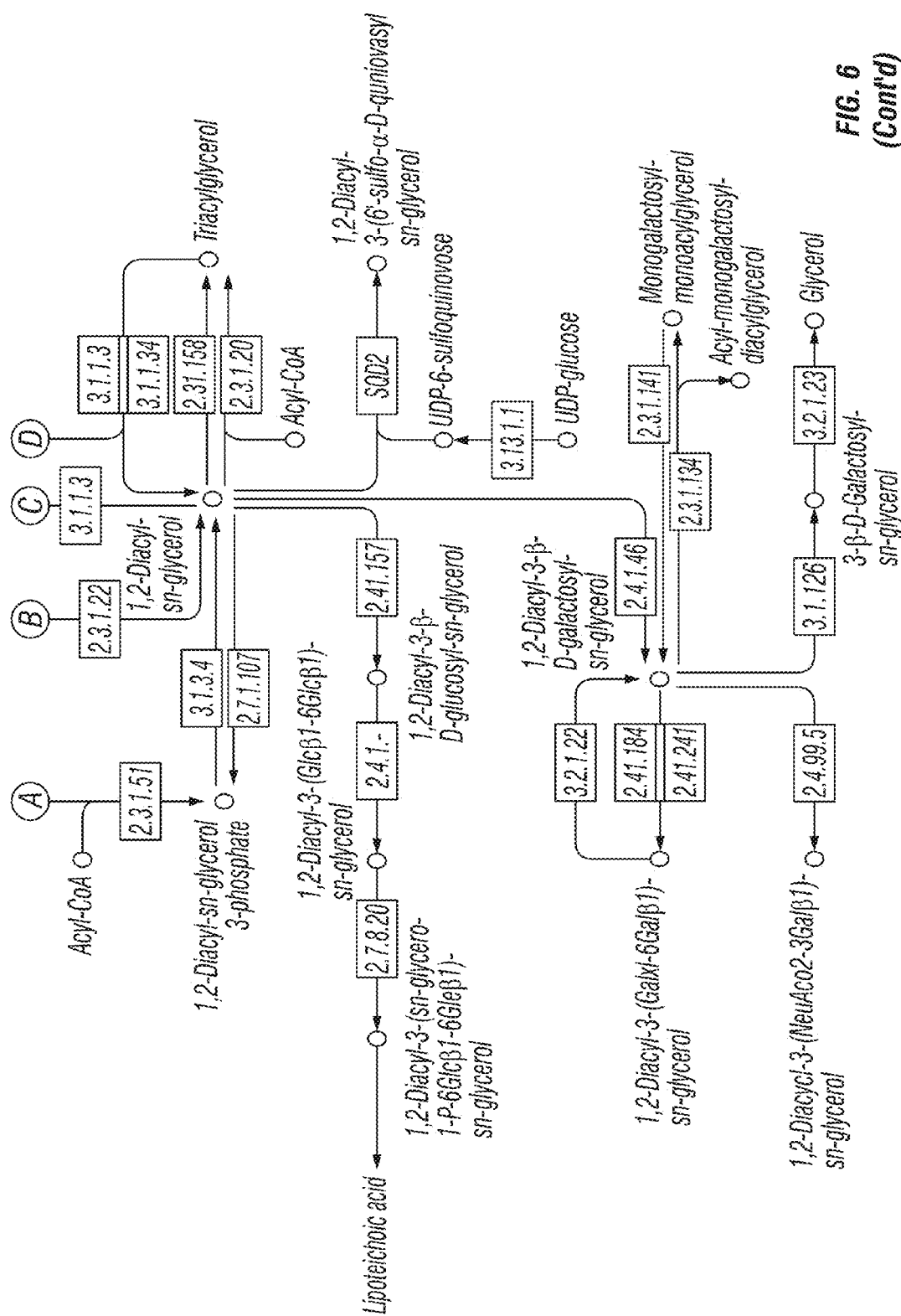


FIG. 5B





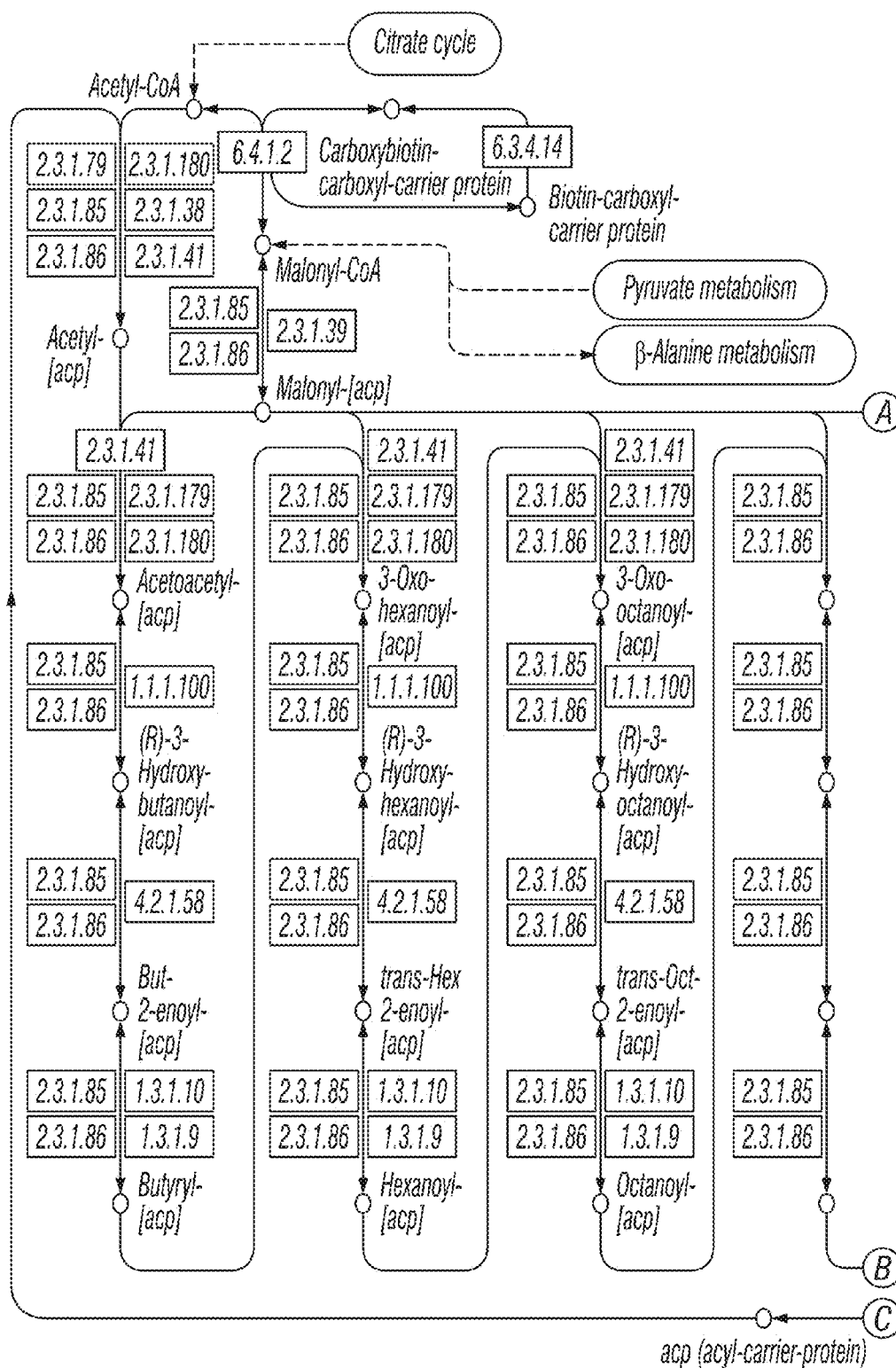
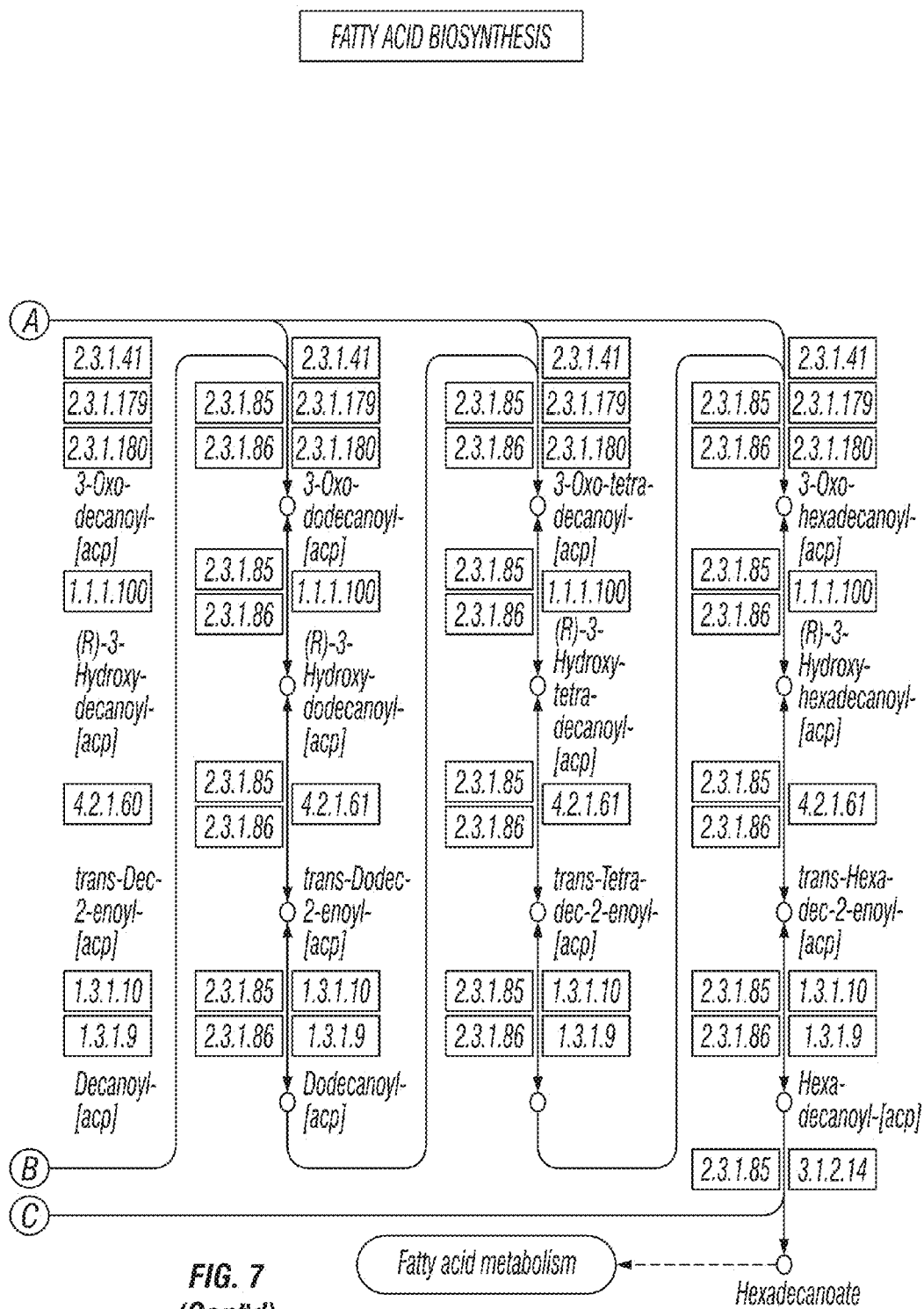
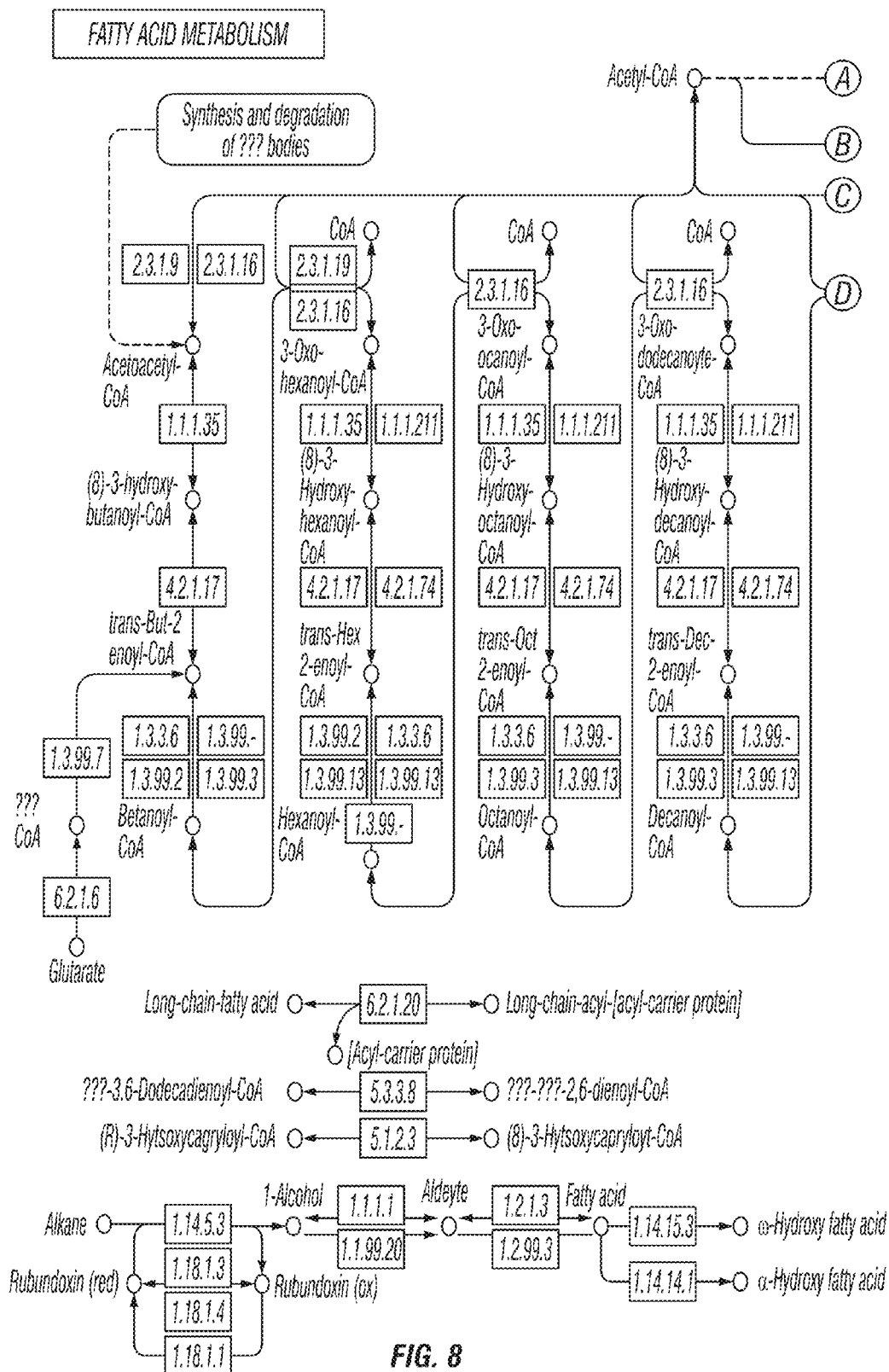


FIG. 7





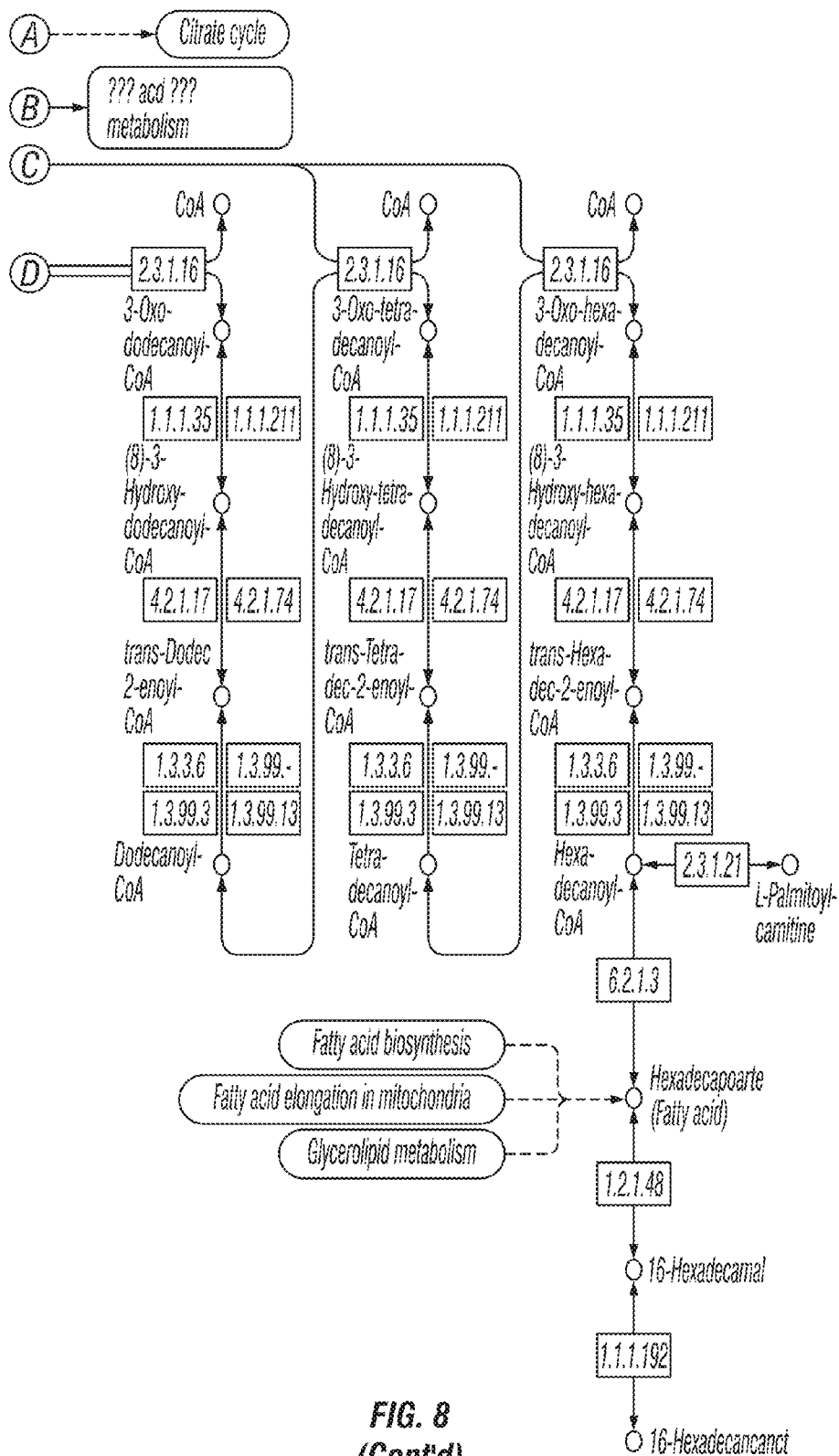


FIG. 8
(Cont'd)

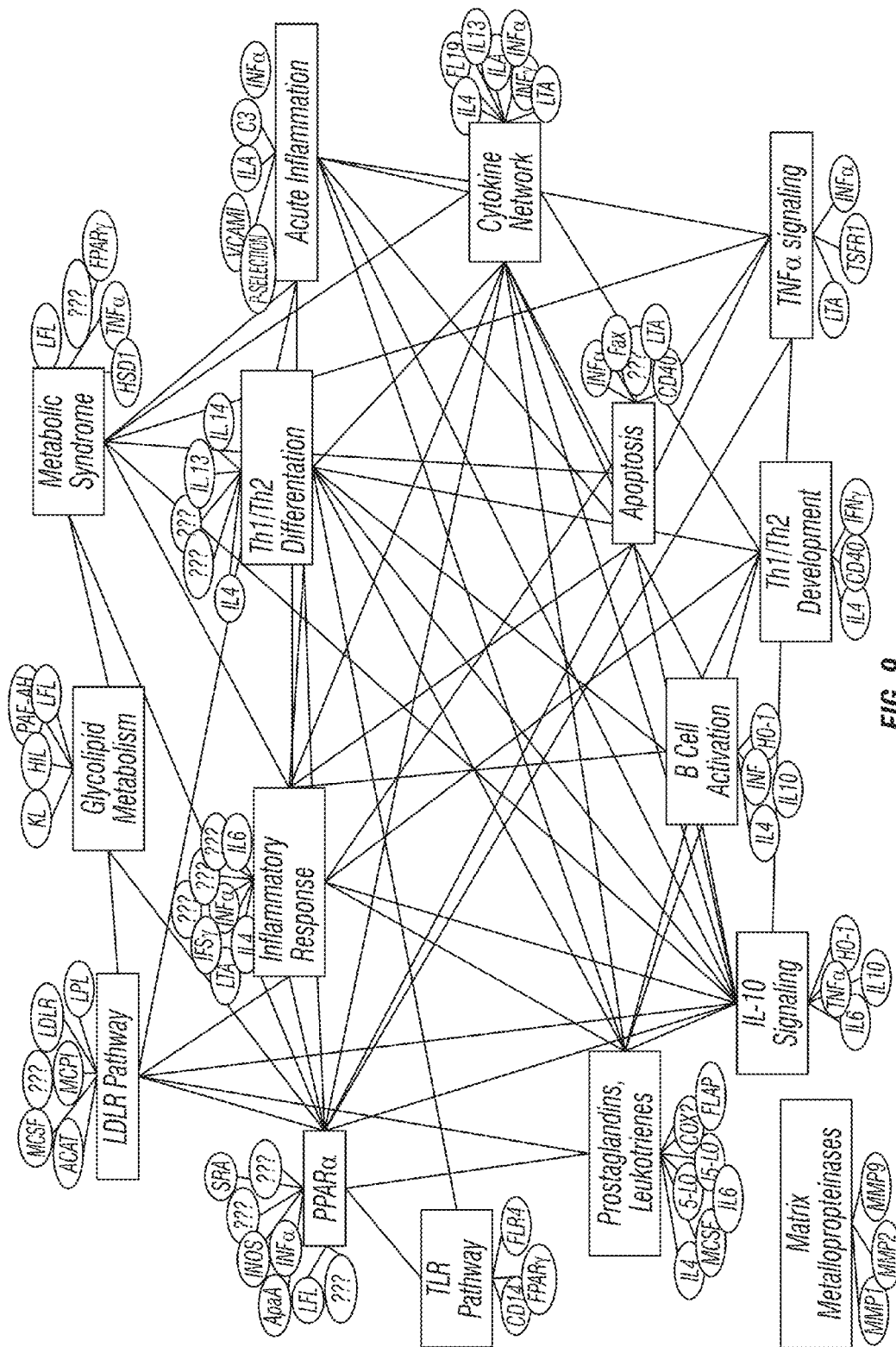


FIG. 9

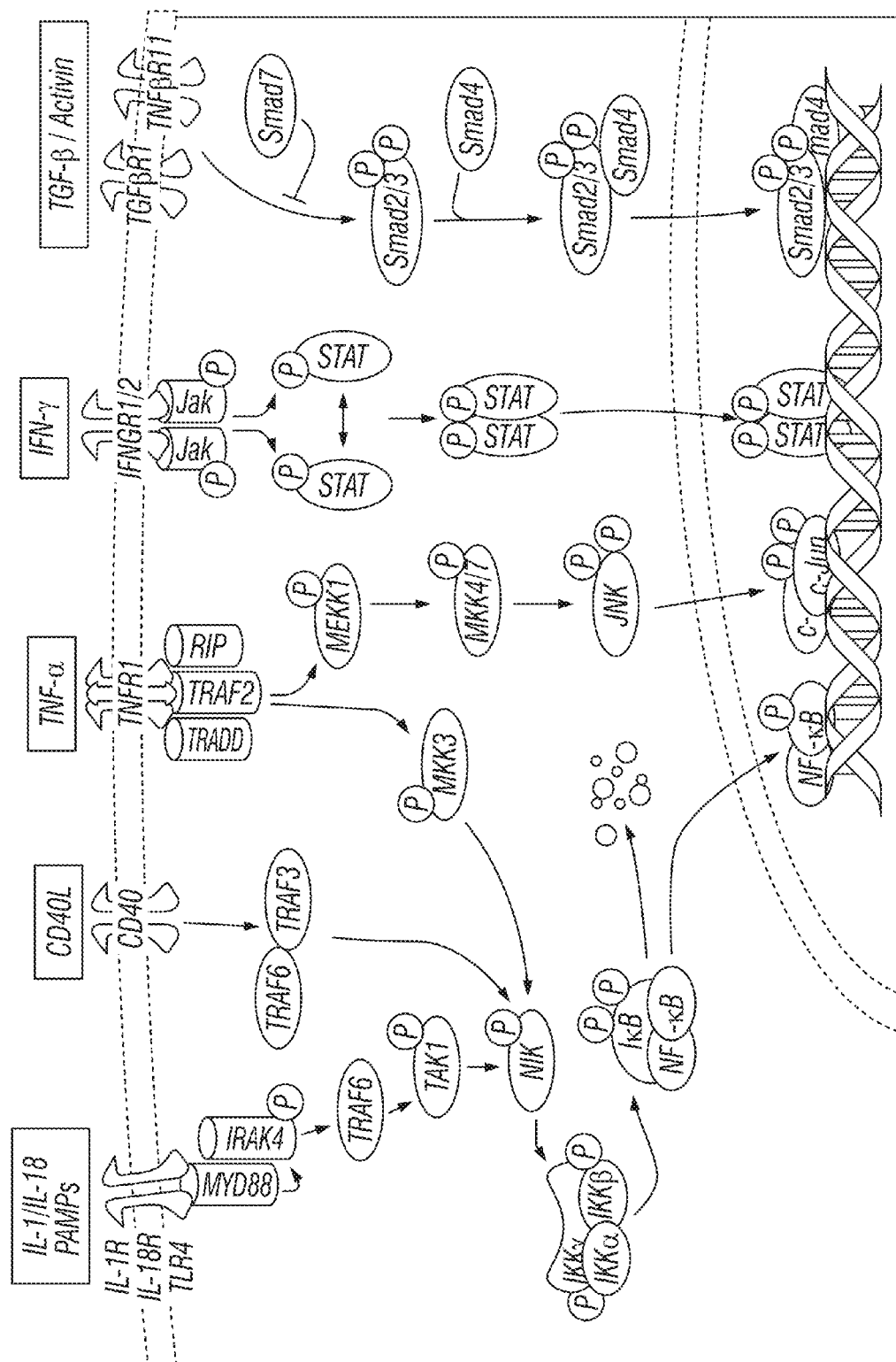


FIG. 10

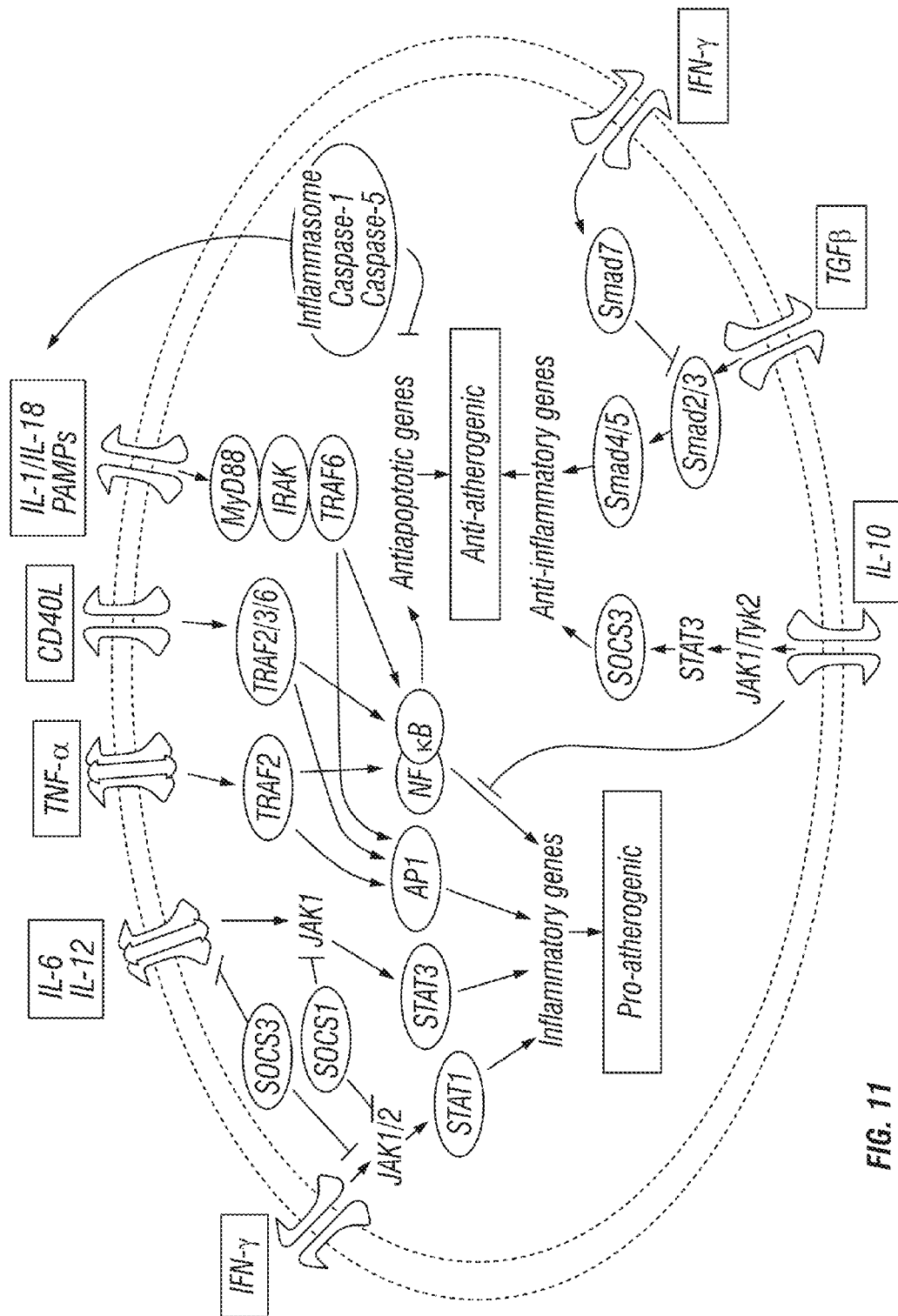


FIG. 11

1

MODELS OF ATHEROSCLEROSIS, HYPERLIPIDEMIA, LIPOPROTEIN OXIDATION AND BLOOD VESSEL INFLAMMATION AND METHODS FOR MAKING AND USING THEM

TECHNICAL FIELD

This invention relates to molecular and cellular biology, biochemistry, molecular genetics, gene therapy, and drug design and discovery. In one aspect, the invention is directed to genetically altered fish of the family Cyprinidae, or genus *Danio*, including zebrafish (*Danio rerio*) and host cells and cell lines from these animals, where the fish have been genetically altered to lack or have a modified gene related to lipid metabolism, for example, an apolipoprotein E (ApoE), apolipoprotein A-I (ApoAI) and/or a low density lipoprotein receptor (LDL-R) gene. In another aspect, the invention is directed to drug design or discovery using the animal or cell models of the invention and/or wild type zebrafish, and by administering an altered diet and/or environment to the animal of invention.

BACKGROUND

Atherosclerosis is an inflammatory disease of blood vessels resulting in the growth of deposits of fatty substances, cholesterol, cellular waste products, calcium and other substances in the inner lining of an artery. This buildup is called plaque. It usually affects large and medium-sized arteries. Plaques can grow large enough to significantly reduce the blood flow through an artery. But most of the damage occurs when they become fragile and rupture. Plaques that rupture cause blood clots that can block blood flow or break off and travel to another part of the body. If either happens and blocks a blood vessel that feeds the heart, it causes a heart attack. If it blocks a blood vessel that feeds the brain, it causes a stroke.

Atherosclerosis starts when high content of cholesterol in the blood (hypercholesterolemia) leads to the lipid accumulation in the artery wall. This can start even in the fetus if the mother is hypercholesterolemic and progresses during the lifetime. Lipid accumulated in the artery wall undergoes oxidation and attracts inflammatory cells, monocytes, which differentiate into macrophages and take up the lipid. Resulting lipid-loaded macrophage "foam" cells residing in the artery inner layer (intima) are a hallmark of early atherosclerotic lesions. They further contribute to chronic vascular inflammation and the plaque growth. Therefore, studying the mechanisms of macrophage recruitment, lipid uptake and inflammation is important for understanding the pathogenesis of atherosclerosis. A feasible in vivo model of vascular lipid accumulation and inflammation will be also valuable for drug discovery.

Hyperlipidemia and hypercholesterolemia are developed as a consequence of an altered expression of genes regulating lipid metabolism and/or an altered dietary intake of lipids. In mammals, apolipoprotein E (ApoE), apolipoprotein A-I (ApoAI) and low density lipoprotein receptor (LDL-R) are critical proteins that regulate metabolism of lipoproteins, although many other genes are involved.

Current animal models of atherosclerosis: In an effort of establishing animal models of atherosclerosis researchers recreate in animals two major causative factors of the disease in humans, high cholesterol content in blood and high blood pressure. The latter is achieved by administration of high doses of angiotensin. However, the most popular models of atherosclerosis are the ones that achieve high levels of cho-

2

lesterol in plasma. There are two animal species currently used to model atherosclerosis, hypercholesterolemic rabbits and genetically modified mice. Mouse models are especially widely utilized due to the availability of many transgenic and knockout strains.

Feeding atherosclerosis-susceptible mouse strains (C57BL/6) high-fat, high-cholesterol diet causes the development of a very minimal atherosclerotic disease. However, this is greatly accelerated and increased in the mice deficient of either of two genes, which encode the proteins responsible for normal lipid delivery, the low-density lipoprotein receptor (LDLR) and apolipoprotein E (ApoE). The LDLR is on the surface of eventually every cell in the body; it recognizes LDL particles and, via the LDL uptake, the cells get nutrients, including fatty acids and cholesterol. ApoE is a part of lipoprotein particles and it also participates in the cellular uptake of lipid nutrients. The absence of either LDLR or ApoE, combined with the feeding a high-fat, high cholesterol diet, leads to the accumulation of high levels of LDL (the major carrier of cholesterol in blood) in plasma and eventually to its accumulation in artery wall and atherosclerosis.

Thus, LDLR^{-/-} or ApoE^{-/-} mice placed on high-fat diets are currently the two major animal models of atherosclerosis. Although having numerous advantages, these mouse models also have important limitations: A. Relatively long periods of pregnancy, maturation and cholesterol feeding, total from 6 to 12 months; B. A relatively high cost of maintaining of a mouse colony and numerous regulations for the handling of the mammals; C. A complex and labor intensive morphological analysis of atherosclerotic lesions; D. Atherosclerotic lesions in most cases can be analyzed only postmortem, e.g. at one time point only. Existing live animal imaging techniques are inadequate, of low resolution and often use radioactive materials.

SUMMARY

The invention provides stably genetically altered fish of the family Cyprinidae comprising at least one gene of lipid metabolism, such as genetically altered ApoE, ApoAI and/or LDL-R gene locus. The invention provides fish that have been genetically altered to lack or have a modified gene related to lipid metabolism; the genes can be e.g., an ApoE, ApoAI and/or LDL-R gene. In one aspect, the fish is of the family *Danio*, e.g., a zebrafish (*Danio rerio*). The invention provides isolated or cultured cells or tissues, or cell lines, derived from the fish of the invention. In one aspect, the gene or a set of genes related to lipid metabolism, e.g., the ApoE, ApoAI and/or LDL-R gene locus, are completely or partially knocked out in any combination; for example, in one aspect, only the ApoE, ApoAI and/or LDL-R are completely or partially knocked out, or alternatively some or all of these, or other lipid metabolism genes, are also completely or partially knocked out.

The invention provides stably genetically altered fish of the family Cyprinidae comprising or consisting of (a) an exogenous gene or a set of genes related to lipid metabolism, including the genes and/or polypeptides (or the sequence encoding them) illustrated or referenced in FIG. 6, FIG. 7, FIG. 8 and/or FIG. 9; (b) at least one gene from a genetically (sequence) altered ApoE, ApoAI and/or LDL-R gene locus; (c) a deleted, or "knocked out" homologous gene or a set of genes related to lipid metabolism; (d) the fish of (a) or (c), wherein the gene or a set of genes related to lipid metabolism comprise or consist of an ApoE, ApoAI and/or LDL-R gene; or (e) any combination of (a) to (d).

In one aspect, at least one nucleic acid residue of the gene or a set of genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus, is altered or removed, or one or several heterologous sequences is/are inserted into the gene or a set of genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus, or an endogenous sequence is rearranged in the gene or a set of genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus. In one aspect, the gene or a set of genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus is modified such that no or less amount of gene or a set of genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R, message (transcript) and/or polypeptide is expressed. In one aspect, the gene or a set of genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus, is modified such that the polypeptides, e.g., ApoE, ApoAI and/or LDL-R polypeptides, have no or less or altered activity.

The invention provides methods and/or models for studying the biology or pathology of lipoprotein metabolism and atherosclerosis or any inflammation associated with lipid accumulation, or for finding compounds capable of ameliorating or preventing or reversing: atherosclerosis; hyperlipidemia; lipoprotein oxidation; the accumulation of lipid in a blood vessel wall; vascular inflammation associated with lipid accumulation in a blood vessel wall; acute atherosclerosis-associated events; heart attack; stroke; or a combination thereof, comprising: maintaining a fish of the family Cyprinidae under conditions comprising an altered diet and/or environmental conditions conducive to initiating or maintaining accumulation of lipid in a blood vessel wall of the fish, or conditions conducive to initiating or maintaining atherosclerosis. In one aspect, the altered diet comprises a high fat diet (an enriched fat diet). In one aspect, the altered diet comprises a high cholesterol diet (an enriched cholesterol diet). In one aspect, the altered diet comprises a fluorescently labeled lipid. In one aspect, the fish is a wild type or a genetically altered fish of any one of the invention.

The invention provides methods for screening for a compound capable of ameliorating or preventing or reversing: atherosclerosis; hyperlipidemia; lipoprotein oxidation; the accumulation of lipid in a blood vessel wall; vascular inflammation associated with lipid accumulation in a blood vessel wall; acute atherosclerosis-associated events; heart attack; stroke, comprising: (a) providing a test compound; (b) administering the test compound to (i) a genetically altered fish of any one of the invention; (ii) a fish of the family Cyprinidae under conditions comprising an altered diet and/or environmental conditions conducive to initiating or maintaining hyperlipidemia, lipoprotein oxidation, accumulation of lipid in a blood vessel wall of the fish, or conditions conducive to initiating or maintaining atherosclerosis; or (iii) the genetically altered fish of (i) under the diet and/or environmental conditions of (ii); (c) determining if the test compound ameliorates, prevents and/or reverses atherosclerosis and/or the accumulation of lipid in a blood vessel wall and/or vascular inflammation associated with lipid accumulation in a blood vessel wall. In one aspect, the test compound is a small molecule, a polypeptide, a peptide, a nucleic acid, an siRNA, a polysaccharide or a lipid. In one aspect, the test compound is designed to target and/or increase or decrease the activity of: a matrix metalloproteinase, a lipoxygenase, a cyclooxygenase a phospholipase, a toll-like receptor, a NADPH oxidase, a nuclear receptor, a transcription factor NF- κ B associated gene expression, macrophage lipid uptake, endothelial adhesion molecules and/or monocyte recruitment, smooth muscle cell growth and migration, apoptosis of vascular cells,

phagocytosis of apoptotic cells, activation of T- and B-1 cells in the lesions, or a combination thereof.

Also provided herein are kits comprising cells of the invention including instructions for practicing the methods provided herein.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

All publications, patents, patent applications, GenBank sequences and ATCC deposits, cited herein are hereby expressly incorporated by reference for all purposes.

DESCRIPTION OF DRAWINGS

FIG. 1(A) illustrates data showing the total cholesterol (TC) and triglycerides (TG) in the plasma of a normal zebrafish and the zebrafish fed a high-cholesterol diet, as measured using automated enzymatic assays, as described in detail, below. FIG. 1(B) illustrates data from an immunoassay used to detect oxidized phospholipids in LDL and in HDL in the plasma of a normal zebrafish and the zebrafish fed a high-cholesterol diet, as described in detail, below.

FIG. 2 illustrates a confocal microscope image of cholesterol accumulation in the vasculature of a zebrafish, as described in detail, below.

FIG. 3 illustrates a confocal microscope image of disturbed endothelial cell morphology in the dorsal aorta of a zebrafish fed high-cholesterol diet, as described in detail, below; FIG. 3A and FIG. 3C are the images of dorsal aorta of a control and a high-cholesterol fed larva; FIG. 3B and FIG. 3D are the 3D images of the same aorta segments.

FIG. 4 illustrates a confocal microscope image of macrophage accumulation and cholesterol uptake in the dorsal aorta of a zebrafish larva, as described in detail, below.

FIG. 5(A) illustrates a microscope image showing that the addition of ezetimibe in the fish tank water considerably reduced a level of cholesterol accumulated in the digestive system of a zebrafish; the FIG. 5(B) illustrates images that demonstrate that ezetimibe prevented pathological changes in the endothelial layer morphology of the zebrafish, as inflicted by a high fat diet, as described in detail, below.

FIG. 6, FIG. 7 and FIG. 8 illustrate lipid-related metabolic pathways and their enzymes, including a glycerolipid metabolism pathway, a fatty acid biosynthesis pathway, and fatty acid metabolism, respectively, and set forth exemplary enzymes (including their fish homologues, or counterparts) that can be used to practice this invention.

FIG. 9 illustrates an atherosclerosis pathway interaction network, and shows a schematic representation of interactions between 16 biological and metabolic pathways that contain genes associated with atherosclerosis, and one or several of these polypeptide and/or genes, including their fish homologues (counterparts), can be used to practice this invention.

FIG. 10 illustrates signaling pathways involved in atherogenesis, and one or several of these polypeptide and/or genes, including their fish homologues (counterparts), can be used to practice this invention.

FIG. 11 illustrates genes and proteins, e.g., enzymes, involved in cross-talks between proinflammatory/proatherogenic and anti-inflammatory/antiatherogenic signal transduction pathways, and one or several of these polypeptide and/or genes, including their fish homologues (counterparts), can be used to practice this invention.

Like reference symbols in the various drawings indicate like elements.

DETAILED DESCRIPTION

The invention provides a novel fish (e.g., zebrafish) model to study mechanisms of and finding therapies against hyperlipidemia, lipoprotein oxidation, accumulation of lipid in the blood vessel wall and associated inflammation, including vascular inflammation. These processes can be rate-limiting steps in the formation of atherosclerotic lesions in humans and further promote the advanced lesion development, which may eventually result in heart attack or ischemic stroke, the two major causes of mortality in developed countries. Thus, the invention provides a model to study mechanisms of and finding therapies against (e.g., compositions and methods for the amelioration of) atherosclerotic lesions in humans, heart attack or ischemic stroke, hyperlipidemia, lipoprotein oxidation, accumulation of lipid in the blood vessel wall and associated inflammation, including vascular inflammation.

In one aspect, the invention provides stable genetically altered fish of the family Cyprinidae comprising or consisting of (a) an exogenous gene or a set of genes related to lipid metabolism, e.g., as set forth in FIG. 6, FIG. 7, FIG. 8, FIG. 9, FIG. 10 and/or FIG. 11; (b) at least one gene from a genetically (sequence) altered ApoE, ApoAI and/or LDL-R gene locus; (c) a deleted, or “knocked out” homologous gene or a set of genes related to lipid metabolism; (d) the fish of (a) or (c), wherein the gene or a set of genes related to lipid metabolism comprise or consist of an ApoE, ApoAI and/or LDL-R gene; or (e) any combination of (a) to (d). FIG. 9 illustrates an atherosclerosis pathway interaction network, and shows a schematic representation of interactions between sixteen biological and metabolic pathways that contain genes associated with atherosclerosis, and one or several of these genes, including their fish homologues (counterparts), can be used to practice this invention. The connections between the pathways illustrate the presence of common atherosclerosis genes in two pathways. IL-10, interleukin-10; LDLR, LDL receptor; PPAR α , peroxisome proliferator-activated receptor α ; Th1/Th2, T helper cell 1/2; TLR, toll-like receptor; TNF- α , tumor necrosis factor- α ; genes encoding these proteins, including their fish homologues (counterparts), also can be used to practice this invention.

FIG. 10 illustrates signaling pathways involved in atherogenesis, and one or several of these polypeptide and/or genes, including their fish homologues (counterparts), can be used to practice this invention; for example, genes encoding the following can be manipulated in the genetically altered fish of this invention: proinflammatory cytokines (IL-1, IL-18) and pathogens (represented as pathogen-associated molecular patterns, PAMP), as well as nonpathogen activators of TLR, act through distinct signaling pathways that converge on the activation of NF- κ B; MyD88 functions as an adaptor between receptors of the TLR or IL-1R families and downstream signaling kinases; following association of MyD88 with IL-1-associated kinase IRAK-4, IRAK-4 is autophosphorylated, dissociates from the receptor complex, and interacts with TNF-receptor-associated factor-6 (TRAF-6), which also mediates CD40 signaling; once activated, TRAF6 associates with the MAP3 kinase TAK1 (716); from TAK1, two signaling pathways diverge; one ultimately leads to NF- κ B activation and the other to MAP kinase activation; in its inactive form, NF- κ B is bound to inhibitor of κ B (IK- κ B α / β) in the cytoplasm and consists of an LB kinase (IKK) complex containing two kinases IKK α and IKK β , and the regulatory protein IKK γ (also named NEMO); IKK activation initiates

IkB α / β phosphorylation; phosphorylated LB is then ubiquitinated, leading to its degradation by the 26S proteasome; this releases NF- κ B dimers from the cytoplasmic NF- κ B-IkB complex, allowing them to translocate to the nucleus. JNK phosphorylation is mediated by two MAPK kinases (MAP-KKs), MKK4 and MKK7, that they can cooperatively activate JNK. Both kinases are required for full activation of JNK by environmental stressors, and MKK7 is essential for JNK activation by TNF engagement. Tyrosine phosphorylation activates the cytosolic inactive STATs, resulting in their nuclear translocation and gene activation. This pathway was originally found to be activated by IFNs, but a number of cytokines, growth factors, and hormonal factors also activate JAK and/or STAT proteins. IFN- γ utilizes JAK1 and JAK2, and usually activates STAT1. TGF- β -triggered signals are transduced by proteins belonging to the Smad (for vertebrate homologs of Sma and Mad) family. The type I receptor recognizes and phosphorylates Smad2 and Smad3, which associates with Smad4, forming complexes that participate in DNA binding and recruitment of transcription factors. Smad3 may also have antagonistic properties, as it plays a critical role in TGF- β -dependent repression of vascular inflammation by inhibiting AP-1 activity. Smad7 inhibits Smad2 and Smad3 phosphorylation. See, e.g., Tedgui et al., *Physiol. Rev.* 86: 515-581, 2006.

FIG. 11 illustrates genes and proteins, e.g., enzymes, involved in cross-talks between proinflammatory/pro-atherogenic and anti-inflammatory/antiatherogenic signal transduction pathways, and one or several of these polypeptide and/or genes, including their fish homologues (counterparts), can be used to practice this invention; for example, genes encoding the following can be manipulated in the genetically altered fish of this invention: inhibitory Smads such as Smad7 downstream of IFN- γ signaling associate with activated receptors and interfere with Smad2 and Smad3 binding; IFN- γ , the anti-inflammatory cytokine IL-10 also activates JAK and/or STAT proteins; IL-10/IL-10R interaction activates JAK1 and Tyk2, leading to STAT3 and SOCS3 activation, which is central for the anti-inflammatory responses of IL-10 in macrophages; an inflammasome may be a central link between apoptosis and inflammation in pathological conditions; NF- κ B may have a dual role in atherosclerosis, being pro-atherogenic through its proinflammatory properties, and antiatherogenic through its anti-apoptotic activities. See, e.g., Tedgui et al., *Physiol. Rev.* 86: 515-581, 2006.

In one aspect, a zebrafish model of atherosclerosis is generated by altering dietary and environmental conditions and/or a genetic background of zebrafish. Examples of such alterations are high cholesterol diet and ApoE knockdown:

1. Feeding zebrafish with a diet enriched with cholesterol leads to lipid accumulation in blood vessels and atherosclerosis. Addition of a fluorescently labeled lipid facilitates visualizing the lipid accumulation in blood vessels.

2. Knockdown of ApoE, combined with high-cholesterol diet, accelerates and/or increases atherosclerosis burden in zebrafish.

3. Development of vascular inflammation and atherosclerosis is observed in an optically transparent zebrafish with fluorescent vasculature (fli:EGFP) and in real time using a fluorescent microscope.

In one aspect, the methods of the invention are practiced using optical transparency. Optical transparency of zebrafish makes it a unique model for a real-time, multiparametric in vivo study of the processes involved in atherosclerosis. In addition, the models of this invention make screening of drug candidates for atherosclerosis therapy feasible and cost effective.

The fish and cells of the invention, e.g., zebrafish, provide models for various developmental, physiological and pathological processes. The use of fish and cells of the invention are optimal for the development of a model of atherosclerosis for the following reasons:

A. A zebrafish embryo/larva is optically transparent for up to 30 days, which allows conducting real time microscopic observations in a live animal. Zebrafish can be easily genetically modified. For example, in a transgenic zebrafish strain with enhanced green fluorescence protein (EGFP) constitutively expressed in endothelial cells (the cells that cover the inner surface of blood vessels), fli:EGFP, vascular system is readily visualized under a fluorescent microscope.

B. A zebrafish colony maintenance is by far more economic than the maintenance of a mouse colony.

C. New drug candidates can be easily tested in a zebrafish model by simply adding them to the water in a fish tank. This makes zebrafish an ultimate in vivo model for new drug development.

D. Zebrafish embryo feeds from yolk for the first 5 days post fertilization and is free feeding thereafter. The yolk sac constantly forms lipoproteins, which then gain entry into circulation and supply nutrients to the tissues. Remarkably, zebrafish ApoE, which is homologous to human and mouse ApoE, is highly expressed in the yolk sac. This suggests that the mechanisms of lipoprotein delivery are similar in zebrafish and in mammals, and regulated manipulation with these processes gains a suitable model for atherosclerosis, a disease originating from disturbed lipid metabolism.

Thus, this invention provides applications of finding therapeutic targets and pre-clinical testing of the therapies to prevent and/or slow down the development of atherosclerosis. The potential targets may include but not limited to:

- macrophage matrix metalloproteinases,
- 12/15-lipoxygenase,
- 5-lipoxygenase,
- toll-like receptors 2 and 4,
- NF-kappaB associated gene expression,
- macrophage lipid uptake,
- endothelial adhesion molecules and monocyte recruitment,
- smooth muscle cell growth and migration,
- apoptosis of vascular cells,
- phagocytosis of apoptotic cells,
- activation of T- and B-1 cells in the lesions, and many others.

Feasibility and low cost of the zebrafish model, together with its access to real-time imaging of atherosclerotic processes in a live animal, make it an attractive object for commercial applications.

In another aspect of the invention, a nucleic acid used to practice the invention, including any gene or genes related to lipid metabolism e.g., a ApoE, ApoAI and/or LDL-R gene locus, an expression vector used to insert or express any gene or genes related to lipid metabolism, such as a ApoE, ApoAI and/or LDL-R gene locus, in a cell, cell line, or a fish of the invention, or any target sequence, can comprise a reporter or a marker gene (including nucleic acid sequences that encode proteins that can be used for reporting activity, e.g., enzymes or epitopes). In one aspect, the reporter or marker gene is used to monitor gene (e.g., an ApoE, ApoAI and/or LDL-R gene locus) expression, e.g., one, several or all coding sequence in the locus can be marked with the same or different markers. In one aspect, the reporter or marker gene is used to monitor gene suppression or silencing. In one aspect of the invention, the reporter gene comprises green fluorescent protein. Any

compound, fluorophore, label, isotope, protein or gene that has a reporting or marking function can be used in the methods provided herein.

In another aspect of the invention, nucleic acids used to practice the invention, including any gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus, an expression vector, or any target sequences are inserted into the genome of a host cell by e.g. a vector, a virus or any nucleic acid shuttling or insertional mechanism. For example, a nucleic acid sequence can be inserted into a genome or a vector by a variety of procedures. In one aspect, the sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated. In one aspect, viral long terminal repeats (LTRs) are inserted in a flanking pattern to effect insertion of a desired sequence (e.g., ApoE, ApoAI and/or LDL-R and/or another gene locus) into a genome. In one aspect, sequences homologous to a genome target sequence (targeting where in the genome it is desired to insert a desired nucleic acid, e.g., ApoE, ApoAI and/or LDL-R and/or another gene locus) are inserted in a flanking pattern to effect insertion of the desired sequence into a genome. A variety of cloning techniques are known in the art, e.g., as described in Ausubel and Sambrook. Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector used to make or practice the invention can be chosen from any number of suitable vectors known to those skilled in the art, including cosmids, YACs (Yeast Artificial Chromosomes), megaYACs, BACs (Bacterial Artificial Chromosomes), PACs (P1 Artificial Chromosome), MACs (Mammalian Artificial Chromosomes), a whole chromosome, or a small whole genome. The vector also can be in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, non-chromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by, e.g., Sambrook. Particular bacterial vectors which can be used include the commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017), pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden), GEM1 (Promega Biotec, Madison, Wis., USA) pQE70, pQE60, pQE-9 (Qiagen), pD10, psiX174 pBlue-script II KS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene), ptrc99a, pKK223-3, pKK233-3, DR540, pRIT5 (Pharmacia), pKK232-8 and pCM7. Particular eukaryotic vectors include pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other vector may be used as long as it is replicable and viable in the host cell. In one aspect of the invention, target sequences are integrated into genomes using a lentiviral feline immunodeficiency (FIV) vector for the transduction process.

The invention provides a fish comprising deleted or modified gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R) gene loci. In some aspects, the (fish) endogenous gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus, has been completely, or partially, disabled ("knocked out"). Nucleic acids used to practice the invention, including any gene or genes related to lipid metabolism, e.g., the fish ApoE, ApoAI and/or LDL-R gene locus, and vectors comprising this or other

nucleic acids (e.g., including other ApoE, ApoAI and/or LDL-R gene loci segments for making "knockout" animals) can be made, isolated and/or manipulated by, e.g., cloning and expression of cDNA libraries, amplification of message or genomic DNA by PCR, and the like. In practicing the methods of the invention, homologous or exogenous genes (e.g., gene or genes related to lipid metabolism, e.g., such as ApoE, ApoAI and/or LDL-R loci genes) can be modified by manipulating a template nucleic acid, as described herein. The invention can be practiced in conjunction with any method or protocol or device known in the art, which are well described in the scientific and patent literature.

A fish of the invention include both animals having stably inserted exogenous or homologous gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R sequences (e.g., a complete or partial ApoE, ApoAI and/or LDL-R gene locus), unstable genomic inserts, mitochondrial inserts, or episomal inserts, e.g., as artificial chromosomes that are episomal to the endogenous chromosomes of the animal.

The nucleic acids used to practice this invention, whether RNA, iRNA, siRNA, antisense nucleic acid, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed/generated recombinantly. Recombinant polypeptides generated from these nucleic acids can be individually isolated or cloned and tested for a desired activity. Any recombinant expression system can be used, including bacterial, mammalian, yeast, insect or plant cell expression systems.

Alternatively, these nucleic acids can be synthesized in vitro by well-known chemical synthesis techniques, as described in, e.g., Adams (1983) *J. Am. Chem. Soc.* 105:661; Belousov (1997) *Nucleic Acids Res.* 25:3440-3444; Frenkel (1995) *Free Radic. Biol. Med.* 19:373-380; Blommers (1994) *Biochemistry* 33:7886-7896; Narang (1979) *Meth. Enzymol.* 68:90; Brown (1979) *Meth. Enzymol.* 68:109; Beaucage (1981) *Tetra. Lett.* 22:1859; U.S. Pat. No. 4,458,066. Alternatively, nucleic acids can be obtained from commercial sources.

Techniques for the manipulation of nucleic acids, such as, e.g., subcloning, labeling probes (e.g., random-primer labeling using Klenow polymerase, nick translation, amplification), sequencing, hybridization and the like are well described in the scientific and patent literature, see, e.g., Sambrook, ed., *Molecular Cloning: A Laboratory Manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization with Nucleic Acid Probes*, Part I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Another useful means of obtaining and manipulating nucleic acids used to practice the methods of the invention is to clone from genomic samples, and, if desired, screen and re-clone inserts isolated or amplified from, e.g., genomic clones or cDNA clones. Sources of nucleic acid used in the

methods of the invention include genomic or cDNA libraries contained in, e.g., mammalian artificial chromosomes (MACs), see, e.g., U.S. Pat. Nos. 5,721,118; 6,025,155; human artificial chromosomes, see, e.g., Rosenfeld (1997) *Nat. Genet.* 15:333-335; yeast artificial chromosomes (YAC); bacterial artificial chromosomes (BAC); P1 artificial chromosomes, see, e.g., Woon (1998) *Genomics* 50:306-316; P1-derived vectors (PACs), see, e.g., Kern (1997) *Biotechniques* 23:120-124; cosmids, recombinant viruses, phages or plasmids.

In practicing the invention, nucleic acids of the invention or modified nucleic acids of the invention, can be reproduced by amplification. Amplification can also be used to clone or modify the nucleic acids of the invention. Thus, the invention provides amplification primer sequence pairs for amplifying nucleic acids of the invention. One of skill in the art can design amplification primer sequence pairs for any part of or the full length of these sequences.

Amplification reactions can also be used to quantify the amount of nucleic acid in a sample (such as the amount of message in a cell sample), label the nucleic acid (e.g., to apply it to an array or a blot), detect the nucleic acid, or quantify the amount of a specific nucleic acid in a sample. In one aspect of the invention, message isolated from a cell or a cDNA library are amplified.

The skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (see, e.g., *PCR Protocols, A Guide to Methods and Applications*, ed. Innis, Academic Press, N.Y. (1990) and *PCR Strategies* (1995), ed. Innis, Academic Press, Inc., N.Y., ligase chain reaction (LCR) (see, e.g., Wu (1989) *Genomics* 4:560; Landegren (1988) *Science* 241:1077; Barringer (1990) *Gene* 89:117); transcription amplification (see, e.g., Kwoh (1989) *Proc. Natl. Acad. Sci. USA* 86:1173); and, self-sustained sequence replication (see, e.g., Guatelli (1990) *Proc. Natl. Acad. Sci. USA* 87:1874); Q Beta replicase amplification (see, e.g., Smith (1997) *J. Clin. Microbiol.* 35:1477-1491), automated Q-beta replicase amplification assay (see, e.g., Burg (1996) *Mol. Cell. Probes* 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Can-gene, Mississauga, Ontario; see also Berger (1987) *Methods Enzymol.* 152:307-316; Sambrook; Ausubel; U.S. Pat. Nos. 4,683,195 and 4,683,202; and Sooknanan (1995) *Biotechnology* 13:563-564).

The sequences of the nucleic acids, e.g., the genes or messages (mRNA), related to lipid metabolism, for example, an ApoE, ApoAI and/or LDL-R gene or message, used to practice this invention are well known in the art; for example:

In one aspect, human (*Homo sapiens*) apolipoprotein E (ApoE) sequences can be used (either from complete or partial genomic (gene) or mRNA, or message, sequence) to practice this invention, e.g., in one aspect, human ApoE sequence is inserted into an animal model or cell or cell line of this invention as an exogenous sequences; e.g., in one aspect, all or part of the message for human ApoE is used:

(SEQ ID NO: 1)

```

1  gggtactcttg agtcctactc agccccagcg gaggtgaagg acgtccttcc ccaggagccg
61  actggccaat cacaggcagg aagatgaagg ttctgtgggc tgcgttgctg gtcacattcc
121  tggcaggatg ccaggccaag gtggagcaag cgggtggagac agagccggag cccgagctgc
181  gccagcagac cgagtggcag agcggccagc gctgggaact ggcaactgggt cgcttttggg
241  attacctgcg ctgggtgcag aactgtgtg agcagggtgca ggaggagctg ctcagctccc
301  aggtcaccca ggaactgagg gcgctgatgg acgagaccat gaaggagtgt aaggcctaca

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361 aatcggaact ggaggaacaa ctgaccccg tggcggagga gacgcgggca cggctgtcca
421 aggagctgca ggcggcgag gcccggtgg gcgcggacat ggaggacgtg tgcggccgcc
481 tgggtcagta ccgcgcgag gtgcaggcca tgctcgcca gagcaccgag gagctgcggg
541 tgcgcctcgc ctcccactg cgcaagctgc gtaagcggt cctcccgat gccgatgacc
601 tgcagaagcg cctggcagtg taccaggcgg gggcccgga gggcgccgag cgcggcctca
661 gcgccatccg cgagcgctg gggccctgg tgaacaggg ccgcgtgcgg gccgccactg
721 tgggtccct gccggccag ccgctacagg agcgggcccc ggctggggc gagcggctgc
781 gcgcgcggat ggaggagat ggcagccgga ccgcgacgg cctggacgag gtgaaggagc
841 aggtggcgga ggtgcgcgc aagctggagg agcaggcccc gcagatacgc ctgcaggccg
901 aggccttcca gcccgcctc aagagctggt tcgagccct ggtggaagac atgcagcgcc
961 agtgggcccg gctggtggag aaggtgcagg ctgccgtggg caccagcgcc gccctgtgc
1021 ccagcgacaa tcaactaac cggaagcctg cagccatgag accccacgcc accccgtgcc
1081 tctgcctcc gcgcagcctg cagcgggaga cctgtcccc gccccagcgg tctcctggg
1141 gtggacccta gtttaataaa gattcaccaa gtttcacgca aaaaaaaaa aaaaaaaaa
1201 aaaaaaaaa aaaaaaaaa aaa

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Alternatively, all or part of a sequence encoding human ApoE is used, e.g., the human ApoE amino acid sequence can be:

```

(MSEQ ID NO: 2)
MKVLWAALLVTF LAGCQAKVEQAVETEPEPELRQQTEWQSGQRWELALGR
FWDYLRWVQTLSEQVQEELLSSQVTQELRALMDETMKELKAYKSELEEQL
TPVAEETRARLSKELQAAQARLGADMEDVCGRVLVQYRGEVQAMLGQSTEE
LVRVLASHLRKLRKRLRLDADDLQKRLAVYQAGAREGAERGLSAIRERLG
PLVEQGRVRAATVGSAGQPLQERAQAWGERLRRMEEMGSRTDRDLDEV
KEQVAEVRAKLEEQAQQIRLQAEAFQARLKSWEPLVEDMQRWAGLVEK
VQAAVGTSAAPVPSDNH

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In one alternative aspect, *Danio rerio* (zebrafish) apolipoprotein E (ApoE) sequences are used (either from complete or partial genomic (gene) or mRNA, or message, sequence) to practice this invention, e.g., in one aspect, zebrafish ApoE sequence is modified, knocked out, or modified and re-inserted into an animal model or cell or cell line of this invention as an altered (modified, mutated) endogenous sequence (including deletions, additions, base substitutions), or as an exogenous sequence; e.g., in one aspect, all or part of the message for zebrafish ApoE is used:

```

(MSEQ ID NO: 3)
1 atcaacatga ggtctcttgt ggtattcttt gccctggcag ttttaactgg tgcacaggct
61 cgtagcctgt tccaggctga tgccctcag ccagatggg aggagatggt ggaccgttcc
121 tggcagtatg tgtctgaact caacacacaa actgacggca tggtgcaaaa catcaagggc
181 tcccagctca gcagagagct tgacacacta attactgaca ccatggctga actgagctca
241 tacagtgaat atctccaaac ccagatgacc ccatatgcct ctgatgtgc tggtcagctc
301 agtaaagatc ttcagctcct ggctggaaaa ctccaaactg acatgaccga cgctaaggaa
361 cgcagcactc agtacctgca agagctgaag accatgatgg agcaaaatgc agatgacgtg
421 aagaaccgtg tcggcaccta cacacgcaa ctgaagaaac gctgaacaa ggacacagag
481 gagatccgca acaccgtagc aacctacatg agtgagatgc agtcccgccg tccccaaat
541 gctgatgcag tgaaggaccg tttccagcca tacatgagcc agggccagga tggcgccacc

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601 cagaaactgg gcgccattag cgagctgatg aaggcccagg cgcaggaggt gagcgagcag
 661 ttggagggtcc aggtcggagc tctgaaggag aagctggagg agacagccga gaacctacgc
 721 acctctctgg agggccgtgt ggatgagctg accagcctcc tcgcccccta ctcacagaag
 781 atccgcgagc agctgcagga agtcatggac aagatcaagg aggccacagc agctcttccc
 841 actcaggctt aagagctcca cacttaccta gtgttaacac caaacagaaa gaagaaggga
 901 ggcttttgtgt tactgaaatg tgcttttttc attctgtgag aggttgataa agtggttaac
 961 aactggactc aattggacta gcactgtcct ttactggaca aaagaaatgc catgttactc
 1021 accacgttta ctttctcagt attaacccat gtctgaggat atatttctgt tagcgtacag
 1081 tagagcgaat ttaagatcaa tcaacttgtc tgtcttgagg gctatttttt ctagttagtg
 1141 gggccaaact tggcgctcatt caaaataaat agtaataaaa aggtgccttc agctgctgaa
 1201 atgaatcaga acacatgaaa gatgagcttt gttagtcaac agtcacata taaatgcttg
 1261 ttacttttac atgtttgtgc actgatgtgt ttgaatttgt ttgcaataaa tgtgcgttct
 1321 actacacaaa aaaaaaaaaa aaaaa

In one aspect, all or part of a sequence encoding zebrafish
 ApoE is used, e.g., the zebrafish ApoE amino acid sequence
 can be:

(SEQ ID NO: 4)
 MRSLVVFFALAVLTGCQARSLFQADAPQPRWEEMVDRFWQYVSELNTQTD
 GMVQNIKGSQLSRELDTLITDTMAELSSYSENLTQMTPYASDAAGQLSK
 DLQLLAGKLQTDMDAKERSTQYLQELKTMMEQNADDVKNRVGTYTRKLK
 KRLNKDTEEIRNTVATYMSSEMQRASQNADAVKDRFPYMSQAQDGATQK

25

LGAISELKMQAQEVSEQLVQAGALKEKLEETAENLRTSLEGRVDELTS
 LLAPYSQKIREQLQEVMDKIKEATAALPTQA

30

35

In one aspect, human (*Homo sapiens*) apolipoprotein A-I
 (ApoAI) sequences can be used (either from complete or
 partial genomic (gene) or mRNA, or message,
 sequence) to practice this invention, e.g., in one aspect,
 human ApoAI sequence is inserted into an animal model
 or cell or cell line of this invention as an exogenous
 sequences; e.g., in one aspect, all or part of the message
 for human ApoAI is used:

(SEQ ID NO: 5)

1 agagactgcg agaaggaggt ccccccacggc ccttcaggat gaaagctgcg gtgctgacct
 61 tggccgtgct cttcctgacg gggagccagg ctcggcattt ctggcagcaa gatgaacccc
 121 cccagagccc ctgggatcga gtgaaggacc tggccactgt gtacgtggat gtgctcaaac
 181 acagcggcag agactatgtg tccagtttg aaggctccgc cttgggaaaa cagctaaacc
 241 taaagctcct tgacaactgg gacagcgtga cctccacctt cagcaagctg cgcgacacagc
 301 tcggccctgt gacccaggag ttctgggata acctggaaaa ggagacagag ggcttgaggc
 361 aggagatgag caaggatctg gaggaggtga aggccaaagt gcagccctac ctggacgact
 421 tcgagaagaa gtggcaggag gagatggagc tctaccgcca gaaggtggag ccgctgcgcg
 481 cagagctcca agaggcgcg cgccagaagc tgcacgagct gcaagagaag ctgagccccc
 541 tgggcgagga gatgcgcgac cgcgcgcgcg cccatgtgga cgcgctgcgc acgcatctgg
 601 cccctacag cgacgagctg cgccagcgtt tggccgcgcg ccttgaggct ctcaaggaga
 661 acggcggcgc cagactggcc gactaccacg ccaaggccac cgagcatctg agcacgctca
 721 gcgagaagcg caagcccgcg ctcgaggacc tccgccaagg cctgctgccc gtgctggaga
 781 gcttcaaggc cagcttctcg agcgtctctg aggagtacac taagaagctc aacccccagt
 841 gaggcgcccc ccgcccggc ccttcccggg gctcagaata aacgtttcca aagtggg

15

In one aspect, all or part of a sequence encoding human ApoAI is used, e.g., the human ApoAI amino acid sequence can be:

(SEQ ID NO: 6)

MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVDVLKDSG

RDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLEQLGPVTQEFWDNLE

KETEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMLYRQKVEPLRAEL

QEGARQKLHELQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELQRRLAA

5

10

16

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RLEALKENGGARLAIEYHAKATEHLSTLSEKAKPALEDLRQGLLPVLESFK

VSFLSALIEEYTKKLNTQ

In one aspect, human (*Homo sapiens*) LDL-R sequences can be used (either from complete or partial genomic (gene) or mRNA, or message, sequence) to practice this invention, e.g., in one aspect, human LDL-R sequence is inserted into an animal model or cell or cell line of this invention as an exogenous sequences; e.g., in one aspect, all or part of the message for human LDL-R is used:

(SEQ ID NO: 7)

1 cagaggctgc gagcatgggg ccctgggggt ggaaattgctg ctggaccgtc gccttgctcc

61 tcgccgcggc ggggactgca gtggcgaca gatgcgaaag aaacgagttc cagtgcgaag

121 acgggaaatg catctcctac aagtgggtct gcgatggcag cgctgagtcg caggatggct

181 ctgatgagtc ccaggagacg tgcctgtctg tcacctgcaa atccggggag ttcagctgtg

241 ggggcccgtg caaccgctgc attcctcagt tctggagggt cgatggccaa gtggactgcg

301 acaacggctc agacgagcaa ggctgtcccc ccaagacgtg ctcccaggac gaggttcgct

361 gccacgatgg gaagtgcac tctcggcagt tcgtctgtga ctacagaccg gactgcttgg

421 acggctcaga cgaggcctcc tgcccgggtg tcacctgtgg tcccgcagc ttccagtga

481 acagctccac ctgcaccccc cagctgtggg cctgcgacaa cgaccccgac tgcaagatg

541 gctcggatga gtggccgag cgctgtaggg gtctttacgt gttccaaggg gacagtagcc

601 cctgctcggc cttcgagttc cactgcctaa gtggcgagtg catccactcc agctggcgct

661 gtgatgggtg ccccgactgc aaggacaaat ctgacgagga aaactgcgct gtggccacct

721 gtcgccctga cgaattccag tgctctgatg gaaactgcat ccatggcagc cggcagtggt

781 accgggaata tgactgcaag gacatgagcg atgaagttgg ctgcgttaat gtgacactct

841 gcgaggggac caacaagtgc aagtgtcaca gcggcgaatg catcaccctg gacaaagtct

901 gcaacatggc tagagactgc cgggactggt cagatgaacc catcaaagag tgcgggacca

961 acgaatgctt ggacaacaac ggcggctggt cccacgtctg caatgacctt aagatcggtc

1021 acgagtgcct gtgccccgac ggcttccagc tgggtggcca gcgaagatgc gaagatatcg

1081 atgagtgtca ggatcccgac acctgcagcc agctctgctg gaacctggag ggtggctaca

1141 agtgccagtg tgaggaaggc ttccagctgg acccccacac gaaggcctgc aaggctgtgg

1201 gctccatcgc ctacctcttc ttccaccaac ggacagaggt cagggaagatg acgtgggacc

1261 ggagcgagta caccagcttc atccccaacc tgaggaaagt ggtcgtcttg gacacggagg

1321 tggccagcaa tagaatctac tggcttgacc tgtccagag aatgatctgc agcaccagc

1381 ttgacagagc ccacggcgct tcttcctatg acaccgtcat cagcagggac atccaggccc

1441 ccgacgggct ggctgtggac tggatccaca gcaacatcta ctggaccgac tctgtcctgg

1501 gcactgtctc tggttcggat accaaggggc tgaagaggaa aacgttatcc agggagaacg

1561 gctccaagcc aagggccatc gtggtggatc ctgttcatgg cttcatgtac tggactgact

1621 ggggaactcc cgccaagatc aagaaagggg gctgaaatgg tgtggacatc tactcgtgg

1681 tgactgaaaa cattcagtgg ccaatggca tcaccctaga tctcctcagt ggccgcctct

1741 actgggttga ctccaaactt cactccatct caagcatcga tgtcaacggg ggcaaccgga

1801 agaccatctt ggaggatgaa aagaggctgg cccaccctt ctccttgccc gtctttgagg

1861 acaaagtatt ttggacagat atcatcaacg aagccatttt cagtgccaac cgccctcacg

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1921 gttccgatgt caacttgttg gctgaaaacc tactgtcccc agaggatag gttctcttcc
 1981 acaacctcac ccagccaaga ggagtgaact ggtgtgagag gaccacctg agcaatggcg
 2041 gctgccagta tctgtgccto cctgccccgc agatcaaccc cactcgccc aagtttacct
 2101 gcgcctgccc ggacggcatg ctgctggcca gggacatgag gagctgccto acagaggctg
 2161 aggetgcagt ggccaccag gagacatcca cgtcaggct aaaggtcage tccacagcgg
 2221 taaggacaca gcacacaacc acccggcctg tccccgacac cccccgctg cctggggcca
 2281 ccctgggct caccacgggt gagatagtga caatgtctca ccaagctctg ggcgacgttg
 2341 ctggcagagg aaatgagaag aagccagta gcgtgagggc tctgtccatt gtctcccca
 2401 tctgtctcct cgtctctcct tgcctggggg tctctctct atggaagaac tggcggtta
 2461 agaacatcaa cagcatcaac ttgacaacc cgtctatca gaagaccaca gaggatgagg
 2521 tccacatttg ccacaaccag gacggctaca gctaccctc gagacagatg gtcagtctgg
 2581 aggatgacgt ggcgtgaaca

In one aspect, all or part of a sequence encoding human LDL-R is used, e.g., the human LDL-R amino acid sequence can be:

(SEQ ID NO: 8)
 MGPWGKLRWTVALLAAAGTAVGDR CERNEFQCQDGKCSISKWVC
 DGSACQDGSDESQETCLSVTKSGDFSCGGRVNCIPQFWRCDGQVDCD
 NGSDEQGCPPKTCQDEFRCHDGKCSIRQFVCDSDRCLDGSDEASCPVL
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 NCIHGSRCQDREYDCKDMSDEVGVNVTLCCEGPNKFKCHSGECITLDKVC
 NMARDCRDWSEPIKECGTNECLDNGGCSHVCNDLKI GYECLCPDGFQL
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 TVSVADTKGVKRKTLFRENGSKPRAIVDPVHGFMWTDWGTAKIKKGG
 LNGVDIYSLVTENIQWPNGITLDDLSSGRLYWVDSKLHSISSIDVNGNRK
 TILEDEKRLAHPPFLAVFEDKVFWTDI INEAFSANRLTGSVNLLAENL
 LSPEDMVL FHNLTQPRGVNWCERTTLSNGGCQYLCLPAPQINPHSPKFTC
 ACPDGMILLARDMRSCLTEAAAVATQETSTVRLKVSSTAVRTQHTTTRPV
 PDT SRLPGATPGLTTVEIVTMSHQALGDVAGRGNEKKPSSVRALSIVLP I
 VLLVFLCLGVFL LKWNRLKNINSINFDNPVYQKTTEDEVHICHNQDYS
 YPSRQMVSLEDDVA

Other sequences used to practice this invention, including gene or genes corresponding to genes known to affect or be involved in lipid metabolism, including ApoE, ApoAI and/or LDL-R, from other species, including gene or genes affecting or involved in lipid metabolism in fish, e.g., fish from the family Cyprinidae, or genus *Danio*, including zebrafish (*Danio rerio*), can be routinely identified based on structural homology (e.g., sequence identify) and functional similarity with known genes, messages, proteins and sequences.

Cells and Tissues

The invention also provides cells and tissues (e.g., harvested from a fish of the invention) comprising altered, and/or

a complete or partial gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R, gene loci. In one aspect of the invention, cells have gene expression that has been silenced by mutation, sequence deletion, or by transcriptional silencing, e.g., where the endogenous gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R loci genes, are completely or partially silenced by mutation, sequence deletion and/or by transcriptional silencing. In one aspect, cells whose genes have been silenced, e.g., transcriptionally silenced, include plant and animal cells. In one aspect, animal cells include fish cells.

Where appropriate, host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction).

Transgenic and Modified Fish

The invention provides genetically altered fish of the family Cyprinidae comprising at least one gene from a genetically altered gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus, wherein the fish can be of the family *Danio*, e.g., a zebrafish (*Danio rerio*). The transgenic animals can comprise a complete or partial gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene loci, or subsequences thereof, including an expression cassette or vector or a transfected or transformed cell comprising gene or genes related to lipid metabolism, e.g., a ApoE, ApoAI and/or LDL-R gene locus. The invention also provides methods of making and using these transgenic non-human animals.

"Knockout animals" can also be used to practice the methods of the invention. For example, in one aspect, the transgenic or modified fish of the invention comprise a "knockout animal," e.g., a "knockout" engineered not to express an endogenous gene, including any endogenous gene or genes related to lipid metabolism, e.g., the endogenous ApoE, ApoAI and/or LDL-R gene locus, or subsequences thereof. "Knockouts" can be prepared by deletion or disruption by homologous recombination of an endogenous promoter. "Knockout animals" or "Knockout cells" can be used to practice the methods of the invention. In one aspect, endogenous genes in stem cells are "knocked out" before insertion of a heterologous gene or genes related to lipid metabolism, e.g., ApoE, ApoAI and/or LDL-R gene locus, e.g., human or

murine gene or genes related to lipid metabolism. In alternative aspects, stem cells are myeloid, lymphoid, or neural progenitor or precursor cells.

The invention also provides conditional transgenic or knockout fish produced using recombination methods. For example, an exemplary method comprises use of bacteriophage P1 Cre recombinase and flip recombinase from yeast plasmids. These are two non-limiting examples of site-specific DNA recombinase enzymes that cleave DNA at specific target sites (lox P sites for cre recombinase and frt. sites for flip recombinase) and catalyze a ligation of this DNA to a second cleaved site.

Any of the many known ways to modify the genetics (chromosomes, genes) of a fish can be used to make and practice the methods and compositions of the invention, e.g., inserting transgenes into the germ line of zebrafish. See, e.g., Linnet, et al., *Dev Biol.* 1999 Sep. 1; 213(1):207-16, "Transgene expression in zebrafish: A comparison of retroviral-vector and DNA-injection approaches" (transgenic fish that expressed a nuclear-targeted, enhanced, green fluorescent protein (EGFP) gene were produced using both pseudotyped retroviral vector infection and DNA microinjection of embryos); or, Sod, et al., *Methods.* 2006 July; 39(3):220-7, "Methods for reverse genetic screening in zebrafish by resequencing and TILLING" (using a reverse genetic approach that utilizes screening by resequencing and/or TILLING (Targeting Induced Local Lesions IN Genomes) of mutagenized genomes, spermatogonia of healthy males were mutagenized using ENU (N-ethyl-N-nitrosourea) and F1 progeny collected by breeding treated males with healthy wild type females); or, Wienholds, et al., *Genome Res.* 2003 December; 13(12):2700-7, "Efficient target-selected mutagenesis in zebrafish" (making a target-selected knockout in zebrafish using ENU-mutagenized F1 animals).

Drug Discovery

The methods and compositions of the invention can be used in drug discovery. The methods and compositions of the invention can be used for target validation; and, in some applications, can provide a physiologically accurate and less expensive approach to screen potential drugs. Expression arrays can be used to determine the expression of transgenic genes or genes other than a targeted gene or pathway.

The invention provides methods, cells and animals for determining the toxicity and pharmacokinetics of any compound, e.g., drugs, pesticides, herbicides, pollutants, and the like, using the cells and/or a fish of the invention.

Kits and Libraries

The invention provides kits comprising compositions and methods of the invention, including cells and/or fish of the invention, target sequences, transfecting agents, transducing agents, instructions (regarding the methods of the invention), or any combination thereof. As such, kits, cells, vectors and the like are provided herein.

The invention will be further described with reference to the following examples; however, it is to be understood that the invention is not limited to such examples.

EXAMPLES

Example 1

The invention provides an atherosclerosis model in which raising blood levels of cholesterol and other lipids in fish, e.g., zebrafish, leads to the cholesterol and other lipid accumulation in aorta and vascular inflammation.

Exemplary methods for making and using the invention are:

1. Cholesterol Feeding of Zebrafish

Spray cholesterol (4% in ether) on the fish food, let it dry for 2 hours in a fume hood. Collect and keep at 4° C. Feed the fish with high-cholesterol food for 7 days to 8 weeks.

Draw blood from adult zebrafish that was fed control or high-cholesterol diet and test the plasma for the levels of cholesterol, triglycerides and lipoprotein oxidation.

To visualize the lipid in larvae zebrafish, add to the cholesterol ether solution 10 µg/ml of cholesteryl BODIPY 576/589 C11 (Invitrogen, C12681). This fluorescent (red) cholesterol ester is almost exclusively carried in blood by LDL and does not translocate to other membranes, other than upon LDL cellular uptake. Feed fli:EGFP zebrafish with this high-cholesterol diet for one week.

Collect zebrafish blood and test for cholesterol content.

2. ApoE Knockdown

To knockdown ApoE, inject embryos with a morpholino antisense oligo. An ApoE specific morpholino has been designed and ordered from GeneTools:

apoeb-1 CAAAGAATACCACAAGAGACCTCAT (SEQ ID NO: 9)

Test embryos for the ApoE expression using an anti-human ApoE antibody from Biorad (K74180B, goat). This antibody has been demonstrated in our experiments to recognize a zebrafish protein of approximately the same size as human ApoE.

If ApoE knockdown leads to lipid and macrophage accumulation in the blood vessel wall in zebrafish, generate an ApoE knockout zebrafish.

3. Analysis of Vascular Inflammation and Atherosclerosis

Use a fluorescent confocal microscope to image dorsal aorta of a fli:EGFP zebrafish (wild type or ApoE knockdown) that was placed on a high-cholesterol diet, and compare with a control zebrafish that was fed a normal diet.

Visualize using a C1si confocal microscope:

endothelial cell morphology and the morphology of the vessel

accumulation of fluorescent lipid in the artery wall

Generate 3D rendered images of the aorta

Immunohistochemistry of the whole embryo/larva:

macrophages with Mac-3 antibody (BD Pharmingen)

oxidized lipid moieties with MDA-2 antibody (in-house)

phospho-Akt with a rabbit monoclonal antibody (Cell Signaling)

Hoechst 33258 to visualize cell nuclei

Following immunohistochemical staining, image dorsal aorta in a whole fish with a confocal microscope. Then mount the fish, make cross sections and examine individual sections. Compare the 3D rendering from the confocal with the cross sections.

Harvest peritoneal macrophages from mice (either wild type of genetically modified, e.g. 12/15-lipoxygenase deficient), fluorescently label them with CELLTRACKER™ (Invitrogen, Carlsbad, Calif.) and inject intraperitoneally into a zebrafish. Observe macrophage accumulation in the artery wall. This type of experiment will study the role of specific macrophage molecules in promoting inflammation in atherosclerotic lesions. Alternatively, human monocytes can be used for this purpose. Use nucleofection technology to achieve efficient monocyte transfection with either siRNA or transgene of interest.

The following figures demonstrate the effectiveness of this invention: FIG. 1. Hypercholesterolemia and oxidized lipo-

21

proteins in adult zebrafish. Five week old zebrafish were fed a 4% cholesterol-enriched (HCD) or normal (control) diet, eight animals per group, for 8-10 weeks. Animals were euthanized by prolonged exposure to 0.02% Tricaine, and 2 μ l blood was drawn from the heart and immediately diluted in 9 of ice-cold PBS-EDTA. After centrifugation, 1:10 diluted plasma was collected and used for analysis. FIG. 1 (A) Total cholesterol (TC) and triglycerides (TG) in plasma were measured using automated enzymatic assays. *, $p < 0.001$. FIG. 1 (B) The EO6 immunoassay was used to detect oxidized phospholipids in LDL (EO6/apoB) and in HDL (EO6/apoA1). *, $p < 0.05$. The increase in the EO6 reactivity 20-30 fold in the plasma of hyperlipidemic zebrafish is extremely and uniquely high compared to any animal model of atherosclerosis or human patient samples.

FIG. 2. Cholesterol accumulation in zebrafish arteries. Fli:EGFP zebrafish larvae were fed high-cholesterol diet, containing fluorescent (red) cholesterol ester for 7 days. A whole live zebrafish larva was placed under a confocal microscope and images of vasculature were captured. Green endothelial cells help trace blood vessels, which are also stained red due to a high content of cholesterol in blood. Note bright red areas of the artery (arrowhead), which indicate cholesterol accumulation in the artery wall.

FIG. 3. Disturbed endothelial cell morphology in the dorsal aorta of a fish fed high-cholesterol diet. Endothelial cells cover the inside surface of blood vessels and are first exposed to pro-inflammatory effects of the high cholesterol content in blood. Inflamed endothelium attracts leukocytes, which enter the blood vessel wall. These processes disturb endothelial cell morphology. In the fli-EGFP zebrafish strain, endothelial cells constitutively express EGFP, a fluorescent protein readily visualized with a confocal microscope. FIG. 3A and FIG. 3C are the images of dorsal aorta of a control and a high-cholesterol fed larva. Numerous "holes" (arrowhead) presumably are the sites of leukocytes attachment and entry through the endothelial cells.

FIG. 3B and FIG. 3D are the 3D images of the same aorta segments, rendered from several optical sections through the aorta and rotated 90° to see the aorta lumen (highlighted). Irregular lumen morphology in the high-cholesterol fed zebrafish aorta (D) indicates endothelial cell activation and, possibly, leukocyte entry.

22

FIG. 4. Macrophage accumulation and cholesterol uptake in the dorsal aorta of a zebrafish larva. A zebrafish larva was euthanized following 7 days feeding on high fat diet with addition of a fluorescent (red) cholesterol ester. The whole larva was fixed and stained with Mac3 antibody (green). This antibody recognizes mouse macrophages and apparently crossreacts with zebrafish macrophages. Note that green macrophage staining colocalizes with the red cholesterol staining, indicating the uptake of the lipid by macrophages. The lipid-loaded macrophages are a hallmark of human and mouse atherosclerotic lesions.

FIG. 5. Ezetimibe reduces cholesterol absorption in zebrafish intestine (A) and prevents vascular damage (B). Fli:EGFP zebrafish larvae were feeding for 10 days on high fat diet with a fluorescent (red) cholesterol ester, with or without the addition of ezetimibe in the tank water. Ezetimibe, or (3R,4S)-1-(4-fluorophenyl)-3-((3S)-3-(4-fluorophenyl)-3-hydroxypropyl)-4-(4-hydroxyphenyl)-2-azetidinone, is an FDA-approved medicine (marketed as ZETIA™), which inhibits the absorption of cholesterol by the small intestine. As is evident from the significant reduction in the intensity of red fluorescence (A), the addition of ezetimibe in the fish tank water considerably reduced a level of cholesterol accumulated in the digestive system of a zebrafish, which was fed a high fat diet. Remarkably, ezetimibe rescued blood vessels from high fat diet-induced damage. Images in panel B demonstrate that ezetimibe prevented pathological changes in the endothelial layer morphology, inflicted by high fat diet. These data serve as a prove of principal that our novel zebrafish model can be used to screen for drug candidates to prevent and/or stimulate regression of atherosclerotic vascular pathology.

These results demonstrate that the novel fish (e.g., zebrafish) models of the invention for atherosclerosis presents key characteristic features of the atherosclerotic process observed in humans; thus, the compositions, animals and methods of the invention provide highly informative and cost-effective screening of drug candidates for the treatment of atherosclerosis.

A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

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Gln	Lys	Lys	Trp	Gln	Glu	Glu	Met	Glu	Leu	Tyr	Arg	Gln	Lys	Val	Glu	
						135					140					
Pro	Leu	Arg	Ala	Glu	Leu	Gln	Glu	Gly	Ala	Arg	Gln	Lys	Leu	His	Glu	
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Leu	Gln	Glu	Lys	Leu	Ser	Pro	Leu	Gly	Glu	Glu	Met	Arg	Asp	Arg	Ala	
				165					170					175		
Arg	Ala	His	Val	Asp	Ala	Leu	Arg	Thr	His	Leu	Ala	Pro	Tyr	Ser	Asp	
				180				185					190			
Glu	Leu	Arg	Gln	Arg	Leu	Ala	Ala	Arg	Leu	Glu	Ala	Leu	Lys	Glu	Asn	
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Gly	Gly	Ala	Arg	Leu	Ala	Glu	Tyr	His	Ala	Lys	Ala	Thr	Glu	His	Leu	
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Ser	Thr	Leu	Ser	Glu	Lys	Ala	Lys	Pro	Ala	Leu	Glu	Asp	Leu	Arg	Gln	
						230				235					240	
Gly	Leu	Leu	Pro	Val	Leu	Glu	Ser	Phe	Lys	Val	Ser	Phe	Leu	Ser	Ala	
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<210> SEQ ID NO 7
 <211> LENGTH: 2600
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

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ctgatgagtc	ccaggagacg	tgtttgtctg	tcacctgcaa	atccggggac	ttcagctgtg	240
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acaacctcac	ccagccaaga	ggagtgaact	ggtgtgagag	gaccacctg	agcaatggcg	2040
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<210> SEQ ID NO 8
<211> LENGTH: 860
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

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<400> SEQUENCE: 8

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Gln Cys Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly
35        40        45
Ser Ala Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu
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Ser Val Thr Cys Lys Ser Gly Asp Phe Ser Cys Gly Gly Arg Val Asn
65        70        75        80
Arg Cys Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp
85        90        95
Asn Gly Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp
100       105       110
Glu Phe Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys
115       120       125
Asp Ser Asp Arg Asp Cys Leu Asp Gly Ser Asp Glu Ala Ser Cys Pro
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Val Leu Thr Cys Gly Pro Ala Ser Phe Gln Cys Asn Ser Ser Thr Cys
145       150       155       160
Ile Pro Gln Leu Trp Ala Cys Asp Asn Asp Pro Asp Cys Glu Asp Gly
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Ser Asp Glu Trp Pro Gln Arg Cys Arg Gly Leu Tyr Val Phe Gln Gly
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Asp Ser Ser Pro Cys Ser Ala Phe Glu Phe His Cys Leu Ser Gly Glu
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Cys Ile His Ser Ser Trp Arg Cys Asp Gly Gly Pro Asp Cys Lys Asp
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Lys Ser Asp Glu Glu Asn Cys Ala Val Ala Thr Cys Arg Pro Asp Glu
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Val Thr Leu Cys Glu Gly Pro Asn Lys Phe Lys Cys His Ser Gly Glu
275       280       285
Cys Ile Thr Leu Asp Lys Val Cys Asn Met Ala Arg Asp Cys Arg Asp
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Trp Ser Asp Glu Pro Ile Lys Glu Cys Gly Thr Asn Glu Cys Leu Asp
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Asn Asn Gly Gly Cys Ser His Val Cys Asn Asp Leu Lys Ile Gly Tyr

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Val	Asn	Leu	Glu	Gly	Gly	Tyr	Lys	Cys	Gln	Cys	Glu	Glu	Gly	Phe	Gln		
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Ser	Glu	Tyr	Thr	Ser	Leu	Ile	Pro	Asn	Leu	Arg	Asn	Val	Val	Ala	Leu		
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Asp	Thr	Glu	Val	Ala	Ser	Asn	Arg	Ile	Tyr	Trp	Ser	Asp	Leu	Ser	Gln		
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Arg	Met	Ile	Cys	Ser	Thr	Gln	Leu	Asp	Arg	Ala	His	Gly	Val	Ser	Ser		
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Val	Asp	Trp	Ile	His	Ser	Asn	Ile	Tyr	Trp	Thr	Asp	Ser	Val	Leu	Gly		
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Thr	Val	Ser	Val	Ala	Asp	Thr	Lys	Gly	Val	Lys	Arg	Lys	Thr	Leu	Phe		
			500					505					510				
Arg	Glu	Asn	Gly	Ser	Lys	Pro	Arg	Ala	Ile	Val	Val	Asp	Pro	Val	His		
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Gly	Phe	Met	Tyr	Trp	Thr	Asp	Trp	Gly	Thr	Pro	Ala	Lys	Ile	Lys	Lys		
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Gly	Gly	Leu	Asn	Gly	Val	Asp	Ile	Tyr	Ser	Leu	Val	Thr	Glu	Asn	Ile		
	545				550						555				560		
Gln	Trp	Pro	Asn	Gly	Ile	Thr	Leu	Asp	Leu	Leu	Ser	Gly	Arg	Leu	Tyr		
			565					570						575			
Trp	Val	Asp	Ser	Lys	Leu	His	Ser	Ile	Ser	Ser	Ile	Asp	Val	Asn	Gly		
		580					585						590				
Gly	Asn	Arg	Lys	Thr	Ile	Leu	Glu	Asp	Glu	Lys	Arg	Leu	Ala	His	Pro		
		595					600					605					
Phe	Ser	Leu	Ala	Val	Phe	Glu	Asp	Lys	Val	Phe	Trp	Thr	Asp	Ile	Ile		
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Asn	Glu	Ala	Ile	Phe	Ser	Ala	Asn	Arg	Leu	Thr	Gly	Ser	Asp	Val	Asn		
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Leu	Leu	Ala	Glu	Asn	Leu	Leu	Ser	Pro	Glu	Asp	Met	Val	Leu	Phe	His		
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Asn	Leu	Thr	Gln	Pro	Arg	Gly	Val	Asn	Trp	Cys	Glu	Arg	Thr	Thr	Leu		
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Ser	Asn	Gly	Gly	Cys	Gln	Tyr	Leu	Cys	Leu	Pro	Ala	Pro	Gln	Ile	Asn		
		675					680					685					
Pro	His	Ser	Pro	Lys	Phe	Thr	Cys	Ala	Cys	Pro	Asp	Gly	Met	Leu	Leu		
	690					695					700						
Ala	Arg	Asp	Met	Arg	Ser	Cys	Leu	Thr	Glu	Ala	Glu	Ala	Ala	Val	Ala		
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Thr	Gln	Glu	Thr	Ser	Thr	Val	Arg	Leu	Lys	Val	Ser	Ser	Thr	Ala	Val		
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Pro Gly Ala Thr Pro Gly Leu Thr Thr Val Glu Ile Val Thr Met Ser
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His Gln Ala Leu Gly Asp Val Ala Gly Arg Gly Asn Glu Lys Lys Pro
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Ser Ser Val Arg Ala Leu Ser Ile Val Leu Pro Ile Val Leu Leu Val
   785                               790                               795                               800

Phe Leu Cys Leu Gly Val Phe Leu Leu Trp Lys Asn Trp Arg Leu Lys
   805                               810                               815

Asn Ile Asn Ser Ile Asn Phe Asp Asn Pro Val Tyr Gln Lys Thr Thr
   820                               825                               830

Glu Asp Glu Val His Ile Cys His Asn Gln Asp Gly Tyr Ser Tyr Pro
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<210> SEQ ID NO 9
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: antisense oligonucleotide

<400> SEQUENCE: 9

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25

What is claimed is:

1. A method for screening for a compound capable of ameliorating or reversing:

an atherosclerosis or

a vascular inflammation associated with lipid accumulation in a blood vessel wall,
the method comprising:

(a) providing a test compound;

(b) providing a genetically altered fish of the family Cyprinidae of the genus *Danio* having an induced vascular inflammation and atherosclerosis,

wherein the vascular inflammation and atherosclerosis is induced by

growing or subjecting the genetically altered *Danio* fish to an enriched cholesterol diet for a time sufficient to lead to cholesterol or lipid accumulation in an aorta and vascular inflammation,

wherein the genetically altered *Danio* fish is a transgenic having an enhanced green fluorescence protein (EGFP) constitutively expressed in endothelial cells such that the *Danio* fish is optically transparent with a fluorescent vasculature (fl:EGFP), and the *Danio* fish has genetic alterations comprising knockdown of an ApoE, ApoAI and/or LDL-R gene locus;

(c) administering the test compound to the genetically altered *Danio* fish of (b); and

(d) determining if the test compound ameliorates or reverses the induced vascular inflammation or the atherosclerosis in the genetically altered *Danio* fish,

wherein identifying a compound that can ameliorate or reverse the induced vascular inflammation or the atherosclerosis in the genetically altered *Danio* fish, identified the compound as a compound capable of ameliorating or reversing:

an atherosclerosis or

a vascular inflammation associated with lipid accumulation in a blood vessel wall.

2. The method of claim 1, wherein the enriched cholesterol diet further comprises a diet selected from the group consisting of:

a high fat diet,

an enriched fat diet,

and

a combination thereof.

3. The method of claim 1, wherein the test compound is selected from the group consisting of a small molecule, a polypeptide, a peptide, a nucleic acid, an siRNA, a polysaccharide, a lipid and a combination thereof.

4. The method of claim 1, wherein the test compound is designed to target and/or increase or decrease the activity of: a matrix metalloproteinase, a lipoxigenase, a cyclooxygenase, a phospholipase, a toll-like receptor, a NADPH oxidase, a nuclear receptor, a transcription factor NF- κ B associated gene expression, or a combination thereof.

5. The method of claim 1, wherein the test compound is designed to target and/or increase or decrease: macrophage lipid uptake, endothelial adhesion molecules and/or monocyte recruitment, smooth muscle cell growth and migration, apoptosis of vascular cells, phagocytosis of apoptotic cells, activation of T- and B-1 cells in the lesions, or a combination thereof.

6. The method of claim 1, wherein the genetically altered *Danio* fish further comprises:

(a) an expressed exogenous gene or an exogenous set of lipid metabolism genes;

(b) a completely or partially deleted, or "knocked out" endogenous lipid metabolism gene or set of lipid metabolism genes; or

(c) a combination of (a) and (b).

7. The method of claim 1, wherein the genetically altered *Danio* fish is a zebrafish (*Danio rerio*).

8. The method of claim 1, wherein in the genetically altered *Danio* fish the LDL-R gene or gene locus is completely knocked out.

9. The method of claim 1, wherein the ApoE, ApoAI and/or LDL-R gene locus has at least one nucleic acid residue altered or removed.

10. The method of claim 1, wherein the ApoE, ApoAI and/or LDL-R gene locus has an inserted heterologous sequence. 5

11. The method of claim 1, wherein the ApoE, ApoAI and/or LDL-R gene locus has a rearranged endogenous sequence. 10

12. The method of claim 1, wherein the ApoE, ApoAI and/or LDL-R gene locus is modified such that no amount or a less amount of ApoE, ApoAI and/or LDL-R message and/or polypeptide is expressed. 15

13. The method of claim 1, wherein in the ApoE, ApoAI and/or LDL-R gene locus is modified such that an ApoE, ApoAI and/or LDL-R polypeptide has no or less than wild type activity. 20

14. The method of claim 1, wherein the ApoE gene or gene locus is completely knocked out. 25

15. The method of claim 1, wherein in the ApoAI gene or gene locus is completely knocked out.

* * * * *